

## Acknowledgment Receipt:

SUBMISSION TYPE: BIO Sequence Filing

APPLICATION NUMBER: 10055797
FIRST NAMED INVENTOR: David Beach

TITLE OF INVENTION: Methods and Compositions for RNA Interference

ATTORNEY DOCKET NUMBER: GNCA-P03-007

FILE LISTING:

transmittal tranGNCA-P03-007SequenceListing.xml 6333 Bytes sequence-listing GNCA-P03-007SequenceListing.txt 108585 Bytes biotechnology-listing-filing GNCA-P03-007SequenceListingbio.xml 957 Bytes

biotechnology-listing-filing u-bio.dtd 3619 Bytes biotechnology-listing-filing u-bioseq.xsl 6067 Bytes

EFS ID: 18382

FILE SIZE: 33563 Bytes

TIMESTAMP: Fri Sep 27 18:06:12 EDT 2002 MESSAGE DIGEST: 7YpGxUb9HmV40PE0Ow+B4A==

DIGITAL CERTIFICATE HOLDER NAME: cn=Matthew P. Vincent, ou=Registered Attorneys

UPLOAD STATUS: You have successfully uploaded your submission to USPTO



## GNCA-P03-007SequenceListing.txt

GNCA-P03-007SequenceListing.txt SEQUENCE LISTING	_ OCT
110. Hammand et al	PATERILAR
<110> Hammond et al.	A PR
<130> GNCA-P03-007	
<140> 10/055,797 <141> 2002-01-22	
<150> 60/189,739 <151> PCT/US01/08435	
<160> 17	
<170> PatentIn version 3.1	
<210> 1 <211> 5775 <212> DNA <213> Homo sapiens	
<220> <221> CDS <222> (1)(5775) <223>	
<400> 1	40
atg aaa agc cct gct ttg caa ccc ctc agc atg gca ggc ctg cag ctc Met Lys Ser Pro Ala Leu Gln Pro Leu Ser Met Ala Gly Leu Gln Leu 1 5 10	48
atg acc cct gct tcc tca cca atg ggt cct ttc ttt gga ctg cca tgg Met Thr Pro Ala Ser Ser Pro Met Gly Pro Phe Phe Gly Leu Pro Trp 20 25 30	96
caa caa gaa gca att cat gat aac att tat acg cca aga aaa tat cag Gln Gln Glu Ala Ile His Asp Asn Ile Tyr Thr Pro Arg Lys Tyr Gln 35 40 45	144
gtt gaa ctg ctt gaa gca gct ctg gat cat aat acc atc gtc tgt tta Val Glu Leu Leu Glu Ala Ala Leu Asp His Asn Thr Ile Val Cys Leu	192
aac act ggc tca ggg aag aca ttt att gct agt act act cta cta aag Asn Thr Gly Ser Gly Lys Thr Phe Ile Ala Ser Thr Thr Leu Leu Lys	240
65 70 75 80 agc tgt ctc tat cta gat cta ggg gag act tca gct aga aat gga aaa Ser Cys Leu Tyr Leu Asp Leu Gly Glu Thr Ser Ala Arg Asn Gly Lys	288
agg acg gtg ttc ttg gtc aac tct gca aac cag gtt gct caa caa gtg Arg Thr Val Phe Leu Val Asn Ser Ala Asn Gln Val Ala Gln Gln Val	336
tca gct gtc aga act cat tca gat ctc aag gtt ggg gaa tac tca aac Ser Ala Val Arg Thr His Ser Asp Leu Lys Val Gly Glu Tyr Ser Asn	384
115 120 125 cta gaa gta aat gca tct tgg aca aaa gag aga tgg aac caa gag ttt Leu Glu Val Asn Ala Ser Trp Thr Lys Glu Arg Trp Asn Gln Glu Phe 130 135 140	432
act aag cac cag gtt ctc att atg act tgc tat gtc gcc ttg aat gtt Thr Lys His Gln Val Leu Ile Met Thr Cys Tyr Val Ala Leu Asn Val	480
ttg aaa aat ggt tac tta tca ctg tca gac att aac ctt ttg gtg ttt Leu Lys Asn Gly Tyr Leu Ser Leu Ser Asp Ile Asn Leu Leu Val Phe	528
165 170 175 gat gag tgt cat ctt gca atc cta gac cac ccc tat cga gaa ttt atg Page 1	576

						G	NCA-	P03-	007s	eque	nceL	isti	ng.t	xt		
Asp	Glu	Cys	His 180	Leu	Ala										Met	
aag Lys	ctc Leu	tgt Cys 195	gaa Glu	att Ile	tgt Cys	cca Pro	tca Ser 200	tgt Cys	cct Pro	cgc Arg	att Ile	ttg Leu 205	gga Gly	cta Leu	act Thr	624
gct Ala	tcc Ser 210	att Ile	tta Leu	aat Asn	ggg Gly	aaa Lys 215	tgg Trp	gat Asp	cca Pro	gag Glu	gat Asp 220	ttg Leu	gaa Glu	gaa Glu	aag Lys	672
ttt Phe 225	cag Gln	aaa Lys	cta Leu	gag Glu	aaa Lys 230	att Ile	ctt Leu	aag Lys	agt Ser	aat Asn 235	gct Ala	gaa Glu	act Thr	gca Ala	act Thr 240	720
gac Asp	ctg Leu	gtg Val	gtc Val	tta Leu 245	gac Asp	agg Arg	tat Tyr	act Thr	tct Ser 250	cag Gln	cca Pro	tgt Cys	gag Glu	att Ile 255	gtg Val	768
gtg Val	gat Asp	tgt Cys	gga Gly 260	cca Pro	ttt Phe	act Thr	gac Asp	aga Arg 265	agt Ser	ggg Gly	ctt Leu	tat Tyr	gaa Glu 270	aga Arg	ctg Leu	816
ctg Leu	atg Met	gaa Glu 275	tta Leu	gaa Glu	gaa Glu	gca Ala	ctt Leu 280	aat Asn	ttt Phe	atc Ile	aat Asn	gat Asp 285	tgt Cys	aat Asn	ata Ile	864
					gaa Glu											912
cta Leu 305	tca Ser	gac Asp	tgt Cys	cgt Arg	gcc Ala 310	gta Val	ttg Leu	gta Val	gtt Val	ctg Leu 315	gga Gly	ccc Pro	tgg Trp	tgt Cys	gca Ala 320	960
gat Asp	aaa Lys	gta Val	gct Ala	gga Gly 325	atg Met	atg Met	gta Val	aga Arg	gaa Glu 330	cta Leu	cag Gln	aaa Lys	tac Tyr	atc Ile 335	aaa	1008
cat His	gag Glu	caa Gln	gag Glu 340	gag Glu	ctg Leu	cac His	agg Arg	aaa Lys 345	ttt Phe	tta Leu	ttg Leu	ttt Phe	aca Thr 350	gac Asp	act Thr	1056
ttc Phe	cta Leu	agg Arg 355	aaa Lys	ata Ile	cat His	gca Ala	cta Leu 360	tgt Cys	gaa Glu	gag Glu	cac His	ttc Phe 365	tca	cct Pro	gcc Ala	1104
tca Ser	ctt Leu 370	gac Asp	ctg Leu	aaa Lys	ttt Phe	gta Val 375	act Thr	cct Pro	aaa Lys	gta Val	atc Ile 380	aaa Lys	ctg Leu	ctc Leu	gaa Glu	1152
atc Ile 385	tta Leu	cgc Arg	aaa Lys	tat Tyr	aaa Lys 390	cca Pro	tat Tyr	gag Glu	cga Arg	cac His 395	agt Ser	ttt Phe	gaa Glu	agc Ser	gtt Val 400	1200
					aga Arg											1248
Ser	Glu	Asp	Asp 420	Asp	gag Glu	Asp	Glu	Glu 425	Ile	Glu	Glu	Lys	G1u 430	Lys	Pro	1296
Glu	Thr	Asn 435	Phe	Pro	tct Ser	Pro	Phe 440	Thr	Asn	Ile	Leu	Cys 445	Ğly	Ile	Ile	1344
Phe	Va1 450	Ğlu	Arg	Arg	tac Tyr	Thr 455	ĂΊα	۷a٦	۷a٦	Leu	Asn 460	Arg	Leū	Ile	Lyš	1392
gaa Glu 465	gct Ala	ggc Gly	aaa Lys	caa Gln	gat Asp 470	cca Pro	gag Glu	ctg Leu	gct Ala	tat Tyr 475	atc Ile	agt Ser	agc Ser	aat Asn	ttc Phe 480	1440
ata Ile	act Thr	gga Gly	cat His	ggc Gly 485	att Ile	ggg Gly	aag Lys	aat Asn	cag Gln 490	cct Pro	cgc Arg	aac Asn	aac Asn	acg Thr 495	atg Met	1488
Glu	Ala	Glu	Phe 500	Arg	aaa Lys	Gln	Glu	Glu 505	Val	Leu	Arg	Lys	Phe 510	cga Arg	Āla	1536
cat	gag	acc	aac	ctg	ctt	att	gca			att Page		gaa		ggt	gtt	1584

						_	NCA-	n/l2	0076	oauo	ncol	icti	na t	·×+		
ніѕ	Glu	Thr 515	Asn	Leu	Leu			PO3- Thr							val	
gat Asp	ata Ile 530	cca Pro	aaa Lys	tgc Cys	aac Asn	ttg Leu 535	gtg Val	gtt Val	cgt Arg	ttt Phe	gat Asp 540	ttg Leu	ccc Pro	aca Thr	gaa Glu	1632
tat Tyr 545	cga	tcc Ser	tat Tyr	gtt Val	caa Gln 550	tct	aaa Lys	gga Gly	aga Arg	gca Ala 555	agg	gca Ala	ccc Pro	atc Ile	tct Ser 560	1680
aat	tat Tyr	ata Ile	atg Met	tta Leu 565	gcg Ala	gat Asp	aca Thr	gac Asp	aaa Lys 570	ata	aaa Lys	agt Ser	ttt Phe	gaa Glu 575	gaa	1728
gac Asp	ctt Leu	aaa Lys	acc Thr 580	tac	aaa Lys	gct Ala	att Ile	gaa Glu 585	aag	atc Ile	ttg Leu	aga Arg	aac Asn 590	aag	tgt Cys	1776
tcc Ser	aag Lys	tcg Ser 595	gtt	gat Asp	act Thr	ggt Gly	gag Glu 600	act	gac Asp	att Ile	gat Asp	cct Pro 605	gtc	atg Met	gat Asp	1824
gat Asp	gat Asp 610	cac His	gtt Val	ttc Phe	cca Pro	cca Pro 615	tat	gtg Val	ttg Leu	agg Arg	cct Pro 620	gac Asp	gat Asp	ggt Gly	ggt Gly	1872
cca Pro 625	cga Arg	gtc Val	aca Thr	atc Ile	aac Asn 630	acg Thr	gcc Ala	att Ile	gga Gly	cac His 635	atc Ile	aat Asn	aga Arg	tac Tyr	tgt Cys 640	1920
gct Ala	aga Arg	tta Leu	cca Pro	agt Ser 645	gat Asp	ccg Pro	ttt Phe	act Thr	cat His 650	cta Leu	gct Ala	cct Pro	aaa Lys	tgc Cys 655	aga Arg	1968
Thr	Arg	Ğlü	Leu 660	Pro	gat Asp	Ğly	Thr	Phe 665	Tyr	Ser	Thr	Leu	Tyr 670	Leŭ	Pro	2016
Ile	Asn	Ser 675	Pro	Leu	cga Arg	Ala	Ser 680	Ile	Val	Gly	Pro	Pro 685	Met	Ser	Cys	2064
gta Val	cga Arg 690	ttg Leu	gct Ala	gaa Glu	aga Arg	gtt Val 695	gtc Val	gct Ala	ctc Leu	att Ile	tgc Cys 700	tgt Cys	gag Glu	aaa Lys	ctg Leu	2112
cac His 705	aaa Lys	att Ile	ggc Gly	gaa Glu	ctg Leu 710	gat Asp	gac Asp	cat His	ttg Leu	atg Met 715	cca Pro	gtt Val	ggg Gly	aaa Lys	gag Glu 720	2160
act Thr	gtt Val	aaa Lys	tat Tyr	gaa Glu 725	gag Glu	gag Glu	ctt Leu	gat Asp	ttg Leu 730	cat His	gat Asp	gaa Glu	gaa Glu	gag Glu 735	acc Thr	2208
agt Ser	gtt Val	cca Pro	gga Gly 740	aga Arg	cca Pro	ggt Gly	tcc Ser	acg Thr 745	aaa Lys	cga Arg	agg Arg	cag Gln	tgc Cys 750	tac Tyr	cca Pro	2256
Lys	Ala	11e 755	Pro	Glu	tgt Cys	Leu	Arg 760	Asp	Ser	Tyr	Pro	Arg 765	Pro	Āsp	Gln	2304
ccc Pro	tgt Cys 770	tac Tyr	ctg Leu	tat Tyr	gtg Val	ata Ile <i>7</i> 75	gga Gly	atg Met	gtt Val	tta Leu	act Thr 780	aca Thr	cct Pro	tta Leu	cct Pro	2352
					aga Arg 790											2400
					ata Ile											2448
cac His	ttt Phe	cct Pro	gtg Val 820	tac Tyr	aca Thr	cgc Arg	tct Ser	gga Gly 825	gag Glu	gtt Val	acc Thr	ata Ile	tcc Ser 830	att Ile	gag Glu	2496
ttg Leu	aag Lys	aag Lys 835	tct Ser	ggt Gly	ttc Phe	atg Met	ttg Leu 840	tct Ser	cta Leu	caa Gln	atg Met	ctt Leu 845	gag	ttg Leu	att Ile	2544
aca	aga	ctt	cac	cag	tat	ata	ttc	tca		att Page			ctt	gaa	aaa	2592

Thr	Δra	Leu	Hic	Gln	Tyr	G	NCA-	-P03-	-0079	Seque	enc	eLis	stir	1g.1	txt	ı Lys		
	850					855					86	50	_			gtt		2640
Pro 865	Ala	Leu	Glu	Phe	Lys 870	Pro	Thr	Asp	Ala	Asp 875	Se	er A	la	Tyr	Cys	Val 880		2640
cta Leu	cct Pro	ctt Leu	aat Asn	gtt Val 885	gtt Val	aat Asn	gac Asp	tcc Ser	agc Ser 890	Thr	tt L€	g g eu A	at sp	att Ile	gad Asp 895	ttt Phe		2688
aaa Lys	ttc Phe	atg Met	gaa Glu 900	gat Asp	att Ile	gag Glu	aag Lys	tct Ser 905	gaa Glu	gct Ala	C <u>c</u> Ar	gc a gg I	1e	ggc Gly 910	Ιle	ccc Pro		2736
agt Ser	aca Thr	aag Lys 915	tat Tyr	aca Thr	aaa Lys	gaa Glu	aca Thr 920	CCC Pro	ttt Phe	gtt Val	t t Ph	ne L	aa	tta	gaa	gat Asp		2784
Tyr	caa Gln 930	gat Asp	gcc Ala	gtt Val	atc Ile	att Ile 935	cca	aga	tat Tyr	cgc Arg	aa As 94	n P	tt he	gat Asp	caç Glr	cct Pro		2832
	cga	ttt Phe	tat Tyr	gta Val	gct Ala 950	gat	gtg Val	tac Tyr	act Thr	gat Asp 955	ct	t a	cc hr	cca Pro	cto Leu	agt Ser 960		2880
aaa	ttt Phe	cct Pro	tcc Ser	cct Pro 965	gag	tat Tyr	gaa Glu	act Thr	ttt Phe 970	qca	ga G1	u T	at yr	tat Tyr	aaa Lys 975	aca Thr		2928
aag Lys	tac Tyr	Asn	ctt Leu 980	gac	cta Leu	acc Thr	aat Asn	ctc Leu 985	aac	cag Gln	CC Pr	a c	eu	ctg Leu 990	gat	ata		2976
gac Asp	cac His	aca	tct	tca Ser	aga Arg	ctt Leu	aat Asn 100	ct. Lei	t tt	g ac u Th	a c r P	ro /	cga	H	at t is L	tg aa .eu As	at sn	3024
cag Gln		ggg Gly	aaa Lys	gcg Ala	ctt Leu	cct Pro 101	: t	ta ag eu S	gc a er s	gt g er A	ct la	gag	a L	ag i	agg Arg			3069
gcc a	aaa	tgg Trp	gaa Glu			cag	j a	at aa sn Ly				ctg	g V	-	cca Pro			3114
ctc Leu		Ăla	ata Ile			att	C	ca g ro A				tgg	a A		aaa Lys			3159
gtt <sup>.</sup> Val (	tgt	ctc Leu	ccc Pro			ctt	ta I T	at co yr Ai				tgc	C.		ttg Leu			3204
gca (	gag	gag Glu	cta Leu	aga Arg	gcc Ala	cag	a a	ct go hr A	cc ag	gc g er A	sp	gct	g G		gtg Val			3249
gtc a	aga	tca Ser	ctt Leu	cct Pro	gcg Ala	gat	t t	tt ag he Ai	ga ta ng T	ac c yr P	ct ro	aac	t L	ta ( eu /	gac Asp	ttc Phe		3294
ggg 1 Gly	tgg	aaa Lys	aaa Lys			gac	a	gc aa er Ly			tc he	atc	t S		att Ile			3339
aac 1 Asn 5	tcc	tct Ser	tca Ser			aat	g	at aa sp As			gt	aag	H.		agc Ser			3384
att (	gtc	cct Pro	gaa Glu	aat Asn	gct Ala	gca	Ca L H	at ca is G				aat	a A		acc Thr			3429
tct (	cta	gaa Glu	aat Asn			caa	a a	tg to			sn	tgc	a A		acg Thr			3474
ctc a	agc	gag Glu	tcc Ser			aag	C L	tc ca eu H			aa lu	gtt	t S		gca Ala			3519
ctt a			att	aat	ggt			ct ta		at ca Page	aa			tc (	gcc	aat		3564

Section .

						GNC	.v = bU	3-00	7500	u anc	eList	ina	+v+		
Leu	Thr 1175	Ala	Ile	Asn	Glу	Leu 1180	Ser	Tyr	Asn	Gln	Asn 1185	Leu	Ala	Asn	
ggc Gly	agt Ser 1190					aac Asn 1195					caa Gln 1200		aat Asn		3609
	aat Asn 1205					gaa Glu 1210		ccc Pro	gtg Val	caa Gln	cca Pro 1215		acc Thr		3654
	tcc Ser 1220		cag Gln			tac Tyr 1225			gag Glu		cag Gln 1230		cag Gln		3699
	gat Asp 1235					ctg Leu 1240			aaa Lys		ctt Leu 1245		gga Gly		3744
	aac Asn 1250		tct Ser			gat Asp 1255			cct Pro		atg Met 1260		gta Val		3789
	ggt Gly 1265	Thr	Thr	Ăsp	Thr	1270		gtg Val	ctc Leu	aag Lys	ggc Gly 1275		atg Met	~	3834
	gag Glu 1280	Gln	agc Ser	Pro	Ser	Ile 1285	Gly	Tyr	Ser	Ser	agg Arg 1290	Thr	ctt Leu	ĞĨy	3879
	aat Asn 1295	Pro	Gly	Leu	Ile	1300	cag Gln	gct Ala	ttg Leu	act Thr	ctg Leu 1305		aac Asn		3924
ser	gat Asp 1310		ttt Phe			gag Glu 1315					ctt Leu 1320		gac Asp		3969
Phe	tta Leu 1325		cat His			acc Thr 1330					tgc Cys 1335		tac Tyr		4014
	gcg Ala 1340	His	gag Glu	Ğİy	Arg	Leu 1345	Ser	Tyr		Arg	ser 1350		aag Lys		4059
Sér	aac Asn 1355	Cys		Leŭ	Tyr	Arg 1360	Leu	Gly	Lys	Lys	aag Lys 1365		cta Leu		4104
	cgc Arg 1370	Met	۷al	Va1	Ser	1375			ccc Pro				tgg Trp		4149
Pro	Pro 1385	Gly	tat Tyr	۷al	Val	Asn 1390			aaa Lys		aac Asn 1395	Thr	gat Asp	Lys	4194
Trp	1400	Lys	gat Asp	Ğlu	Meť	Thr 1405			tgc Cys			gcg Ala	aat Asn	ggc Gly	4239
Lys	ctg Leu 1415	Ăsp	gag Glu	Ăsp	Tyr	ĞTÜ 1420	Glu	Glu		Glü	G1u 1425		gag Glu		4284
Leū	atg Met 1430	Trp	agg Arg	ĂΊa	Pro	Lys 1435	Ğlu	Ğlü	gct Ala	Āsp	Tyr 1440		gat Asp		4329
Phe	ctg Leu 1445	Glu	tat Tyr	Asp	Gln	Glu 1450	His	Ile	_	Phe	Ile 1455		aat Asn		4374
Leu	меt 1460	Gly	tca Ser	Gly	Αla	Phe 1465	۷al	Lyš	aaa Lys	Ile	Ser 1470	Leu	tct Ser	Pro	4419
ttt Phe	tca Ser 1475	Thr	act Thr	Asp	Ser	Ala 1480			tgg Trp				aaa Lys		4464
tcc	tcc	tta	ggt	agt	atg	cca	ttt	tca	tca Pag	gat ge 5	ttt	gag	gat	ttt	4509

ý . . ·

3...

	GNCA-PO3-007SequenceListing.txt Ser Ser Leu Gly Ser Met Pro Phe Ser Ser Asp Phe Glu Asp Phe															
ser	Ser 1490	Leu	Gly	Ser	Met									Phe		
	tac Tyr 1505	agc Ser	tct Ser	tgg Trp	gat Asp	gca Ala 1510	atg Met				gat Asp 1515		agc Ser		4554	
gct Ala	gtt Val 1520	gaa Glu	gaa Glu	gat Asp	gac Asp	ttt Phe 1525	gtg Val	gtg Val	ggg Gly	ttc Phe	tgg Trp 1530	aat Asn	cca Pro	tca Ser	4599	
		aac Asn	tgt Cys	ggt Gly	gtt Val	gac Asp 1540	acg Thr	gga Gly	aag Lys	cag Gln	tcc Ser 1545	att Ile	tct Ser	tac Tyr	4644	
						tgt Cys 1555							gcg Ala		4689	
_	gtg Val 1565					ggc Gly 1570			tta Leu				ggg Gly		4734	
						ctc Leu 1585					ctg Leu 1590		gtg Val		4779	
	gta Val 1595		aaa Lys						aag Lys		ctg Leu 1605	_	cct Pro		4824	
	gag Glu 1610	aat Asn	ttc Phe	aac Asn	agc Ser	caa Gln 1615	caa Gln				tca Ser 1620		agc Ser		4869	
						agt Ser 1630			tct Ser				aaa Lys		4914	
						aag Lys 1645					tgt Cys 1650		ttt Phe		4959	
	cca Pro 1655					aca Thr 1660					ata Ile 1665		ggg Gly		5004	
	aat Asn 1670					atc Ile 1675					aag Lys 1680		aag Lys		5049	
	ctt Leu 1685					aca Thr 1690					cac His 1695		aat Asn		5094	
_	act Thr 1700	gat Asp	tgt Cys	tac Tyr	cag Gln	cgc Arg 1705	tta Leu	gaa Glu	ttc Phe	ctg Leu	gga Gly 1710	gat Asp	gcg Ala	att Ile	5139	
	gac Asp 1715					aag Lys 1720					gac Asp 1725		cgg Arg		5184	
	tcc Ser 1730	ccg Pro	ggg Gly	gtc Val	ctg Leu	aca Thr 1735	gac Asp	ctg Leu	cgg Arg	tct Ser	gcc Ala 1740	ctg Leu	gtc Val		5229	
	acc Thr 1745					ctg Leu 1750					gac Asp 1755		cac His		5274	
	ttc Phe 1760		gct Ala			cct Pro 1765	gag Glu	ctc Leu	ttc Phe	cat His	gtc Val 1770		gat Asp		5319	
Phe	gtg Val 1775	cag Gln	ttt Phe	cag Gln	ctt Leu	gag Glu 1780	Lys	Asn	Ğlu	Met	caa Gln 1785	gga Gly	atg Met		5364	
	gag Glu 1790	ctt Leu	agg Arg	aga Arg	tct Ser	gag Glu 1795	gag Glu				aaa Lys 1800		gag Glu		5409	
att	gaa	gtt	cca	aag	gcc	atg	ggg	gat		ttt ge 6	gag	tcg	ctt	gct	5454	

```
GNCA-P03-007SequenceListing.txt
Ile Glu Val Pro Lys Ala Met Gly Asp Ile Phe Glu Ser Leu Ala
                                1810
     1805
                                                            1815
ggt gcc att tac atg gat agt ggg atg tca ctg gag
Gly Ala Ile Tyr Met Asp Ser Gly Met Ser Leu Glu
                                                                                         5499
                                                                  aca gtc tgg
                                                                  Thr Val Trp
                                1825
     1820
                                                            1830
cag gtg tac tat ccc atg atg cgg cca cta ata gaa Gln Val Tyr Tyr Pro Met Met Arg Pro Leu Ile Glu
                                                                                         5544
                                                                  aag ttt tct
                                                                  Lys Phe Ser
     1835
                                 1840
                                                            1845
           gta ccc cgt tcc cct gtg cga gaa ttg ctt
Val Pro Arg Ser Pro Val Arg Glu Leu Leu
                                                                                         5589
gca aat
                                                                  gaa atg gaa
Ăla Asn
                                                                  Glu Met Glu
     1850
                                 1855
                                                            1860
           act gcc aaa ttt agc
Thr Ala Lys Phe Ser
                                      ccg gct gag aga act
Pro Ala Glu Arg Thr
                                                                  tac gac ggg
Tyr Asp Gly
cca gaa
                                                                                        5634
Pro Ğlu
     1865
                                 1870
                                                            1875
           aga gtc act gtg gaa
Arg Val Thr Val Glu
                                      gta gta gga aag ggg
Val Val Gly Lys Gly
aag gtc
                                                                  aaa ttt aaa
                                                                                        5679
Lys Val
                                                                  Lys Phe Lys
     1880
                                1885
                                                           1890
ggt gtt ggt cga agt tac agg att gcc aaa tct gca gca aga
Gly Val Gly Arg Ser Tyr Arg Ile Ala Lys Ser Ala Ala Ala Arg
                                                                                        5724
     1895
                                1900
                                                           1905
aga gcc ctc cga agc ctc aaa gct aat caa cct cag
Arg Ala Leu Arg Ser Leu Lys Ala Asn Gln Pro Gln
                                                                 gtt ccc aat
                                                                                        5769
                                                                  Val Pro Asn
     1910
                                1915
                                                            1920
agc tga
                                                                                        5775
Ser
<210>
         1924
<211>
<212>
        PRT
<213>
        Homo sapiens
Met Lys Ser Pro Ala Leu Gln Pro Leu Ser Met Ala Gly Leu Gln Leu 10 15
Met Thr Pro Ala Ser Ser Pro Met Gly Pro Phe Gly Leu Pro Trp
20 25 30
Gln Gln Glu Ala Ile His Asp Asn Ile Tyr Thr Pro Arg Lys Tyr Gln
35 40 45
Val Glu Leu Glu Ala Ala Leu Asp His Asn Thr Ile Val Cys Leu 50 60
Asn Thr Gly Ser Gly Lys Thr Phe Ile Ala Ser Thr Thr Leu Leu Lys 75 80
Ser Cys Leu Tyr Leu Asp Leu Gly Glu Thr Ser Ala Arg Asn Gly Lys
Arg Thr Val Phe Leu Val Asn Ser Ala Asn Gln Val Ala Gln Gln Val
Ser Ala Val Arg Thr His Ser Asp Leu Lys Val Gly Glu Tyr Ser Asn
115 120 125
Leu Glu Val Asn Ala Ser Trp Thr Lys Glu Arg Trp Asn Gln Glu Phe
130 135 140
Thr Lys His Gln Val Leu Ile Met Thr Cys Tyr Val Ala Leu Asn Val
145 150 155 160
```

GNCA-P03-007SequenceListing.txt Leu Lys Asn Gly Tyr Leu Ser Leu Ser Asp Ile Asn Leu Leu Val Phe 165 170 175 Asp Glu Cys His Leu Ala Ile Leu Asp His Pro Tyr Arg Glu Phe Met 180 185 190 Lys Leu Cys Glu Ile Cys Pro Ser Cys Pro Arg Ile Leu Gly Leu Thr 195 200 205 Ala Ser Ile Leu Asn Gly Lys Trp Asp Pro Glu Asp Leu Glu Glu Lys 210 215 220 Phe Gln Lys Leu Glu Lys Ile Leu Lys Ser Asn Ala Glu Thr Ala Thr 225 230 235 240 Asp Leu Val Val Leu Asp Arg Tyr Thr Ser Gln Pro Cys Glu Ile Val 245 250 255 Val Asp Cys Gly Pro Phe Thr Asp Arg Ser Gly Leu Tyr Glu Arg Leu 260 265 270 Leu Met Glu Leu Glu Glu Ala Leu Asn Phe Ile Asn Asp Cys Asn Ile 275 280 285 Ser Val His Ser Lys Glu Arg Asp Ser Thr Leu Ile Ser Lys Gln Ile 290 295 300 Leu Ser Asp Cys Arg Ala Val Leu Val Val Leu Gly Pro Trp Cys Ala 305 310 315 320 Asp Lys Val Ala Gly Met Met Val Arg Glu Leu Gln Lys Tyr Ile Lys 325 330 335 His Glu Glu Glu Leu His Arg Lys Phe Leu Leu Phe Thr Asp Thr 340 345 350 Phe Leu Arg Lys Ile His Ala Leu Cys Glu Glu His Phe Ser Pro Ala 355 360 365 Ser Leu Asp Leu Lys Phe Val Thr Pro Lys Val Ile Lys Leu Leu Glu 370 375 380 Ile Leu Arg Lys Tyr Lys Pro Tyr Glu Arg His Ser Phe Glu Ser Val 385 390 395 400 Glu Trp Tyr Asn Asn Arg Asn Gln Asp Asn Tyr Val Ser Trp Ser Asp 405 410 415 Ser Glu Asp Asp Glu Asp Glu Glu Ile Glu Glu Lys Glu Lys Pro 420 425 430 Glu Thr Asn Phe Pro Ser Pro Phe Thr Asn Ile Leu Cys Gly Ile Ile 435 440 445 Phe Val Glu Arg Arg Tyr Thr Ala Val Val Leu Asn Arg Leu Ile Lys 450 460 Glu Ala Gly Lys Gln Asp Pro Glu Leu Ala Tyr Ile Ser Ser Asn Phe 465 470 480 Ile Thr Gly His Gly Ile Gly Lys Asn Gln Pro Arg Asn Asn Thr Met 485 490 495

GNCA-P03-007SequenceListing.txt Glu Ala Glu Phe Arg Lys Gln Glu Glu Val Leu Arg Lys Phe Arg Ala 500 505 His Glu Thr Asn Leu Leu Ile Ala Thr Ser Ile Val Glu Glu Gly Val 515 525 Asp Ile Pro Lys Cys Asn Leu Val Val Arg Phe Asp Leu Pro Thr Glu 530 540 Tyr Arg Ser Tyr Val Gln Ser Lys Gly Arg Ala Arg Ala Pro Ile Ser 545 550 555 560 Asn Tyr Ile Met Leu Ala Asp Thr Asp Lys Ile Lys Ser Phe Glu Glu 565 570 575 Asp Leu Lys Thr Tyr Lys Ala Ile Glu Lys Ile Leu Arg Asn Lys Cys 580 585 590 Ser Lys Ser Val Asp Thr Gly Glu Thr Asp Ile Asp Pro Val Met Asp 595 600 605 Asp Asp His Val Phe Pro Pro Tyr Val Leu Arg Pro Asp Asp Gly Gly 610 625 Pro Arg Val Thr Ile Asn Thr Ala Ile Gly His Ile Asn Arg Tyr Cys 625 635 640 Ala Arg Leu Pro Ser Asp Pro Phe Thr His Leu Ala Pro Lys Cys Arg 645 650 655 Thr Arg Glu Leu Pro Asp Gly Thr Phe Tyr Ser Thr Leu Tyr Leu Pro 660 665 670 Ile Asn Ser Pro Leu Arg Ala Ser Ile Val Gly Pro Pro Met Ser Cys 675 680 685 Val Arg Leu Ala Glu Arg Val Val Ala Leu Ile Cys Cys Glu Lys Leu 690 695 700 His Lys Ile Gly Glu Leu Asp Asp His Leu Met Pro Val Gly Lys Glu 705 710 715 720 Thr Val Lys Tyr Glu Glu Glu Leu Asp Leu His Asp Glu Glu Glu Thr 725 730 735 Ser Val Pro Gly Arg Pro Gly Ser Thr Lys Arg Arg Gln Cys Tyr Pro 740 745 750 Lys Ala Ile Pro Glu Cys Leu Arg Asp Ser Tyr Pro Arg Pro Asp Gln
755 760 765 Pro Cys Tyr Leu Tyr Val Ile Gly Met Val Leu Thr Thr Pro Leu Pro 770 780 Asp Glu Leu Asn Phe Arg Arg Arg Lys Leu Tyr Pro Pro Glu Asp Thr 785 790 795 800 Thr Arg Cys Phe Gly Ile Leu Thr Ala Lys Pro Ile Pro Gln Ile Pro 805 810 815 His Phe Pro Val Tyr Thr Arg Ser Gly Glu Val Thr Ile Ser Ile Glu 820 825 830

GNCA-P03-007SequenceListing.txt
Leu Lys Lys Ser Gly Phe Met Leu Ser Leu Gln Met Leu Glu Leu Ile
835 840 845 Thr Arg Leu His Gln Tyr Ile Phe Ser His Ile Leu Arg Leu Glu Lys 850 855 860 Pro Ala Leu Glu Phe Lys Pro Thr Asp Ala Asp Ser Ala Tyr Cys Val 865 870 875 880 Leu Pro Leu Asn Val Val Asn Asp Ser Ser Thr Leu Asp Ile Asp Phe 885 890 895 Lys Phe Met Glu Asp Ile Glu Lys Ser Glu Ala Arg Ile Gly Ile Pro 900 905 910 Ser Thr Lys Tyr Thr Lys Glu Thr Pro Phe Val Phe Lys Leu Glu Asp 915 920 925 Tyr Gln Asp Ala Val Ile Ile Pro Arg Tyr Arg Asn Phe Asp Gln Pro 930 935 940 His Arg Phe Tyr Val Ala Asp Val Tyr Thr Asp Leu Thr Pro Leu Ser 945 950 955 960 Lys Phe Pro Ser Pro Glu Tyr Glu Thr Phe Ala Glu Tyr Tyr Lys Thr 965 970 975 Lys Tyr Asn Leu Asp Leu Thr Asn Leu Asn Gln Pro Leu Leu Asp Val 980 985 990 Asp His Thr Ser Ser Arg Leu Asn Leu Leu Thr Pro Arg His Leu Asn 995 1000 1005 Gln Lys Gly Lys Ala Leu Pro Leu Ser Ser Ala Glu Lys Arg Lys 1010 1015 1020 Ala Lys Trp Glu Ser Leu Gln Asn Lys Gln Ile Leu Val Pro Glu 1025 1030 1035 Leu Cys Ala Ile His Pro Ile Pro Ala Ser Leu Trp Arg Lys Ala 1040 1045 1050 Val Cys Leu Pro Ser Ile Leu Tyr Arg Leu His Cys Leu Leu Thr 1055 1060 1065 Ala Glu Glu Leu Arg Ala Gln Thr Ala Ser Asp Ala Gly Val Gly 1070 1080 Val Arg Ser Leu Pro Ala Asp Phe Arg Tyr Pro Asn Leu Asp Phe 1085 1090 1095 Gly Trp Lys Lys Ser Ile Asp Ser Lys Ser Phe Ile Ser Ile Ser 1100 1105 1110Asn Ser Ser Ser Ala Glu Asn Asp Asn Tyr Cys Lys His Ser Thr 1115 1120 1125 Ile Val Pro Glu Asn Ala Ala His Gln Gly Ala Asn Arg Thr Ser 1130 1140 Ser Leu Glu Asn His Asp Gln Met Ser Val Asn Cys Arg Thr Leu 1145 1150 1155 1150

GNCA-P03-007SequenceListing.txt Leu Ser Glu Ser Pro Gly Lys Leu His Val Glu Val Ser Ala Asp Leu Thr Ala Ile Asn Gly Leu Ser Tyr Asn Gln Asn Leu Ala Asn 1175 1180 1185 Gly Ser Tyr Asp Leu Ala Asn Arg Asp Phe Cys Gln Gly Asn Gln 1195 Leu Asn Tyr Tyr Lys Gln Glu Ile Pro Val Gln Pro Thr Thr Ser 1205 1215 Tyr Ser Ile Gln Asn Leu Tyr Ser Tyr Glu Asn Gln Pro Gln Pro 1230 Ser Asp Glu Cys Thr Leu Leu Ser Asn Lys Tyr Leu Asp Gly Asn 1235 1240 1245 1240 Ala Asn Lys Ser Thr Ser Asp Gly Ser Pro Val Met Ala Val Met 1250 1260 Pro Gly Thr Thr Asp Thr Ile Gln Val Leu Lys Gly Arg Met Asp 1265 1270 1275 Ser Glu Gln Ser Pro Ser Ile Gly Tyr Ser Ser Arg Thr Leu Gly Pro Asn Pro Gly Leu Ile Leu Gln Ala Leu Thr Leu Ser Asn Ala 1295 1300 1305 Ser Asp Gly Phe Asn Leu Glu Arg Leu Glu Met Leu Gly Asp Ser 1315 Phe Leu Lys His Ala Ile Thr Thr Tyr Leu Phe Cys Thr Tyr Pro 1325 1330 1335 Asp Ala His Glu Gly Arg Leu Ser Tyr Met Arg Ser Lys Lys Val 1340 Ser Asn Cys Asn Leu Tyr Arg Leu Gly Lys Lys Lys Gly Leu Pro Ser Arg Met Val Val Ser Ile Phe Asp Pro Pro Val Asn Trp Leu 1370 1380 1370 1380 Pro Pro Gly Tyr Val Val Asn Gln Asp Lys Ser Asn Thr Asp Lys 1390 1395 Trp Glu Lys Asp Glu Met Thr Lys Asp Cys Met Leu Ala Asn Gly 1400 1410 Lys Leu\_ Asp Glu Asp Tyr Glu Glu Glu Asp Glu Glu Glu Glu Ser 1415 Leu Met Trp Arg Ala Pro Lys Glu Glu Ala Asp Tyr Glu Asp Asp 1430 1435 1440 Phe Leu\_ Glu Tyr Asp Gln Glu His Ile Arg Phe Ile Asp Asn Met Leu Met Gly Ser Gly Ala Phe Val Lys Lys Ile Ser Leu Ser Pro 1460 1470

GNCA-P03-007SequenceListing.txt Phe Ser Thr Thr Asp Ser Ala Tyr Glu Trp Lys Met Pro Lys Lys 1485 Ser Ser Leu Gly Ser Met Pro Phe Ser Ser Asp Phe Glu Asp Phe 1490 1495 1500 Asp Tyr Ser Ser Trp Asp Ala Met Cys Tyr Leu Asp Pro Ser Lys 1510 Ala Val Glu Glu Asp Asp Phe Val Val Gly Phe Trp Asn Pro Ser 1520 1530 1520 Glu Glu Asn Cys Gly Val Asp Thr Gly Lys Gln Ser Ile Ser Tyr 1535 1540 Asp Leu His Thr Glu Gln Cys Ile Ala Asp Lys Ser Ile Ala Asp 1550 1560 Cys Val Glu Ala Leu Leu Gly Cys Tyr Leu Thr Ser Cys Gly Glu 1565 1570 1575 Arg Ala Ala Gln Leu Phe Leu Cys Ser Leu Gly Leu Lys Val Leu 1580 1590 Pro Val Ile Lys Arg Thr Asp Arg Glu Lys Ala Leu Cys Pro Thr 1595 1600 1605 Arg Glu Asn Phe Asn Ser Gln Gln Lys Asn Leu Ser Val Ser Cys 1610 1615 Ala Ala Ser Val Ala Ser Ser Arg Ser Ser Val Leu Lys Asp 1630 Ser Glu Tyr Gly Cys Leu Lys Ile Pro Pro Arg Cys Met Phe Asp 1640 1645 1650 1640 His Pro Asp Ala Asp Lys Thr Leu Asn His Leu Ile Ser Gly Phe 1655 1660 1665 Glu Asn Phe Glu Lys Lys Ile Asn Tyr Arg Phe Lys Asn Lys Ala 1670 Tyr Leu Leu Gln Ala Phe Thr His Ala Ser Tyr His Tyr Asn Thr 1690 1685 Ile Thr Asp Cys Tyr Gln Arg Leu Glu Phe Leu Gly Asp Ala Ile 1700 1705 1710 Leu Asp Tyr Leu Ile Thr Lys His Leu Tyr Glu Asp Pro Arg Gln 1715 1720 1725 Pro Gly Val Leu Thr Asp Leu Arg Ser Ala Leu Val Asn Asn Thr Ile Phe Ala Ser Leu Ala Val Lys Tyr Asp Tyr His Lys 1745 1750 1755 Tyr Phe Lys Ala Val Ser Pro Glu Leu Phe His Val Ile Asp Asp 1765 Phe Val Gln Phe Gln Leu Glu Lys Asn Glu Met Gln Gly Met Asp 1775 1780

```
GNCA-P03-007SequenceListing.txt
Ser Glu Leu Arg Arg Ser Glu Glu Asp Glu Glu Lys Glu Glu Asp
    1790
                             1795
                                                     1800
Ile Glu Val Pro Lys Ala Met Gly Asp Ile Phe Glu Ser Leu Ala
    1805
                             1810
                                                     1815
Gly Ala Ile Tyr Met Asp Ser Gly Met Ser Leu Glu Thr Val Trp
    1820
                             1825
                                                     1830
Gln Val Tyr Tyr Pro Met Met Arg Pro Leu Ile Glu Lys Phe Ser
    1835
                             1840
                                                     1845
Ala Asn Val Pro Arg Ser Pro Val Arg Glu Leu Leu Glu Met Glu
    1850
                             1855
                                                     1860
Pro Glu Thr Ala Lys Phe Ser Pro Ala Glu Arg Thr Tyr Asp Gly
                                                     1875
    1865
                            1870
Lys Val Arg Val Thr Val Glu Val Val Gly Lys Gly Lys Phe Lys
    1880
                            1885
                                                     1890
Gly Val Gly Arg Ser Tyr Arg Ile Ala Lys Ser Ala Ala Ala Arg
    1895
                            1900
                                                     1905
Arg Ala Leu Arg Ser Leu Lys Ala Asn Gln Pro Gln Val Pro Asn
1910 1915 1920
    1910
ser
<210>
        6750
<211>
<212>
       DNA
<213>
       Drosophila melanogaster
<220>
<221>
       CDS
<222>
        (1)..(6750)
<223>
<400> 3
atg gcg ttc cac tgg tgc gac aac aat ctg cac acc acc gtg ttc acg
                                                                                48
Met Ala Phe His Trp Cys Asp Asn Asn Leu His Thr Thr Val Phe Thr
                                         10
ccg cgc gac ttt cag gtg gag cta ctg gcc acc gcc tac gag cgg aac
Pro Arg Asp Phe Gln Val Glu Leu Leu Ala Thr Ala Tyr Glu Arg Asn
                                                                                96
                                    25
                                                           30
acg att att tgc ctg ggc cat cga agt tcc aag gag ttt ata gcc ctc
                                                                               144
Thr Ile Ile Cys Leu Gly His Arg Ser Ser Lys Glu Phe Ile Ala Leu
                                40
aag ctg ctc cag gag ctg tcg cgt cga gca cgc cga cat ggt cgt gtc
                                                                               192
Lys Leu Leu Gln Glu Leu Ser Arg Arg Ala Arg Arg His Gly Arg Val
    50
                           55
agt gtc tat ctc agt tgc gag gtt ggc acc agc acg gaa cca tgc tcc
Ser Val Tyr Leu Ser Cys Glu Val Gly Thr Ser Thr Glu Pro Cys Ser
65 70 75 80
                                                                               240
atc tac acg atg ctc acc cac ttg act gac ctg cgg gtg tgg cag gag
Ile Tyr Thr Met Leu Thr His Leu Thr Asp Leu Arg Val Trp Gln Glu
                                                                               288
                  85
                                         90
cag ccg gat atg caa att ccc ttt gat cat tgc tgg acg gac tat cac
                                                                               336
Gln Pro Asp Met Gln Ile Pro Phe Asp His Cys Trp Thr Asp Tyr His
              100
                                    105
                                                           110
gtt tcc atc cta cgg cca gag gga ttt ctt tat ctg ctc gaa act cgc
                                                                               384
                                            Page 13
```

_		_						P03-								
		115		•	Pro		120			•		125			_	
gag Glu	ctg Leu 130	ctg Leu	ctg Leu	agc Ser	agc Ser	gtc Val 135	gaa Glu	ctg Leu	atc Ile	gtg Val	ctg Leu 140	gaa Glu	gat Asp	tgt Cys	cat His	432
gac Asp 145	agc Ser	gcc Ala	gtt Val	tat Tyr	cag Gln 150	agg Arg	ata Ile	agg Arg	cct Pro	ctg Leu 155	ttc Phe	gag Glu	aat Asn	cac His	att Ile 160	480
atg Met	cca Pro	gcg Ala	cca Pro	ccg Pro 165	gcg Ala	gac Asp	agg Arg	cca Pro	cgg Arg 170	att Ile	ctc Leu	gga Gly	ctc Leu	gct Ala 175	gga Gly	528
ccg Pro	ctg Leu	cac His	agc Ser 180	gcc Ala	gga Gly	tgt Cys	gag Glu	ctg Leu 185	cag Gln	caa Gln	ctg Leu	agc Ser	gcc Ala 190	atg Met	ctg Leu	576
gcc Ala	acc Thr	ctg Leu 195	gag Glu	cag Gln	agt Ser	gtg Val	ctt Leu 200	tgc Cys	cag Gln	atc Ile	gag Glu	acg Thr 205	gcc Ala	agt Ser	gat Asp	624
att Ile	gtc Val 210	acc Thr	gtg Val	ttg Leu	cgt Arg	tac Tyr 215	tgt Cys	tcc Ser	cga Arg	ccg Pro	cac His 220	gaa Glu	tac Tyr	atc Ile	gta Val	672
					gag Glu 230											720
gtg Val	ctc Leu	aac Asn	aca Thr	cac His 245	aag Lys	tcc Ser	ttt Phe	tta Leu	ttg Leu 250	gac Asp	cac His	cgc Arg	tac Tyr	gat Asp 255	ccc Pro	768
tac Tyr	gaa Glu	atc Ile	tac Tyr 260	ggc Gly	aca Thr	gac Asp	cag Gln	ttt Phe 265	atg Met	gac Asp	gaa Glu	ctg Leu	aaa Lys 270	gac Asp	ata Ile	816
ccc Pro	gat Asp	ccc Pro 275	aag Lys	gtg Val	gac Asp	ccc Pro	ctg Leu 280	aac Asn	gtc Val	atc Ile	aac Asn	tca Ser 285	cta Leu	ctg Leu	gtc Val	864
gtg Val	ctg Leu 290	cac	gag Glu	atg Met	ggt Gly	cct Pro 295	tgg Trp	tgc Cys	acg Thr	cag Gln	cgg Arg 300	gct Ala	gca Ala	cat His	cac His	912
ttt Phe 305	tac Tyr	caa Gln	tgc Cys	aat Asn	gag Glu 310	aag Lys	tta Leu	aag Lys	gtg Val	aag Lys 315	acg Thr	ccg Pro	cac His	gaa Glu	cgt Arg 320	960
cac	tac Tyr	ttg Leu	ctg Leu	tac Tyr 325	tgc Cys	cta Leu	gtg Val	agc Ser	acg Thr 330	gcc Ala	ctt Leu	atc Ile	caa Gln	ctg Leu 335	tac Tyr	1008
tcc Ser	ctc Leu	tgc Cys	gaa Glu 340	cac His	gca Ala	ttc Phe	cat His	cga Arg 345	cat His	tta Leu	gga Gly	agt Ser	ggc Gly 350	agc Ser	gat Asp	1056
tca Ser	cgc Arg	cag Gln 355	acc Thr	atc Ile	gaa Glu	cgc Arg	tat Tyr 360	tcc Ser	agc Ser	ccc Pro	aag Lys	gtg Val 365	cga Arg	cgt Arg	ctg Leu	1104
ttg Leu	cag Gln 370	aca Thr	ctg Leu	agg Arg	tgc Cys	ttc Phe 375	aag Lys	ccg Pro	gaa Glu	gag Glu	gtg Val 380	cac His	acc Thr	caa Gln	gcg Ala	1152
gac Asp 385	gga Gly	ctg Leu	cgc Arg	aga Arg	atg Met 390	cgg Arg	cat His	cag Gln	gtg Val	gat Asp 395	cag Gln	gcg Ala	gac Asp	ttc Phe	aat Asn 400	1200
cgg					ctg Leu											1248
gac Asp	caa Gln	ccg Pro	ccg Pro 420	acg Thr	gag Glu	aca Thr	cga Arg	gcc Ala 425	ctg	gtg Val	gcc Ala	act Thr	ctt Leu 430	gag Glu	cag Gln	1296
att Ile	ctg Leu	cac His 435	acg	aca Thr	gag Glu	gac Asp	agg Arg 440	cag	acg Thr	aac Asn	aga Arg	agc Ser 445	gcc	gct Ala	cgg Arg	1344
gtg	act		act	cct	act	ccc		cat		aag age			cct	agc	tct	1392

						_		503	0076							
val	Thr 450	Pro	Thr	Pro	Thr	Pro 455	NCA- Ala	PU3- His	Ala	eque Lys	nceL Pro 460	Lys	ng.t Pro	xt Ser	Ser	
ggt Gly 465	gcc Ala	aac Asn	act Thr	gca Ala	caa Gln 470	cca Pro	cga Arg	act Thr	cgt Arg	aga Arg 475	cgt Arg	gtg Val	tac Tyr	acc Thr	agg Arg 480	1440
cgc	cac His	cac His	cgg Arg	gat Asp 485	cac	aat Asn	gat Asp	ggc Gly	agc Ser 490	gac Asp	acg Thr	ctc Leu	tgc Cys	gca Ala 495	ctg	1488
att Ile	tac Tyr	tgc Cys	Asn	cag	aac Asn	cac His	acg Thr	Ala	cgc	gtg Val	ctc Leu	ttt Phe	Glu	ctt	cta Leu	1536
gcg Ala	gag Glu	Ile	agc ser	aga Arg	cgt Arg	gat Asp	Pro	505 gat Asp	ctc Leu	aag Lys	ttc Phe	Leu	510 cgc Arg	tgc Cys	cag Gln	1584
tac Tyr	Thr	515 acg Thr	gac Asp	cgg Arg	gtg Val	Ala	520 gat Asp	ccc Pro	acc Thr	acg Thr	gag Glu	525 ccc Pro	aaa Lys	gag Glu	gct Ala	1632
gag Glu 545	ttg Leu	gag Glu	cac His	cgg Arg	cgg Arg 550	cag Gln	gaa Glu	gag Glu	gtg Val	Leu	540 aag Lys	cgc Arg	ttc Phe	cgc Arg	Met	1680
cat	gac Asp	tgc Cys	aat Asn	gtc Val 565	ctg	atc Ile	ggt Gly	act Thr	tcg Ser 570	555 gtg Val	ctg Leu	gaa Glu	gag Glu	Gly	560 atc Ile	1728
gat Asp	gtg Val	ccc Pro	aag Lys 580	tgc	aat Asn	ttg Leu	gtt Val	gtg Val 585	cgc	tgg Trp	gat Asp	ccg Pro	cca Pro 590	acc Thr	aca Thr	1776
tat Tyr	cgc Arg	agt Ser 595	tac	gtt Val	cag Gln	tgc Cys	aaa Lys 600	ggt	cga Arg	gcc Ala	cgt Arg	gct Ala 605	gct	cca Pro	gcc Ala	1824
tat Tyr	cat His 610	gtc	att Ile	ctc Leu	gtc Val	gct Ala 615	ccg	agt Ser	tat Tyr	aaa Lys	agc Ser 620	cca	act Thr	gtg Val	ggg Gly	1872
tca Ser 625	gtg	cag Gln	ctg Leu	acc Thr	gat Asp 630	cgg	agt Ser	cat His	cgg Arg	tat Tyr 635	att	tgc Cys	gcg Ala	act Thr	ggt Gly 640	1920
gat					gac					gat	tca Ser				aac	1968
tcg Ser	tcc Ser	ggc Gly	tcg Ser 660	gat	ccc Pro	tat Tyr	act Thr	ttt Phe 665	ggc	acg Thr	gca Ala	cgc Arg	gga Gly 670	acc	gtg Val	2016
aag Lys	atc Ile	ctc Leu 675	aac	ccc Pro	gaa Glu	gtg Val	ttc Phe 680	agt Ser	aaa Lys	caa Gln	cca Pro	ccg Pro 685	aca	gcg Ala	tgc Cys	2064
		aag					cag				cca Pro 700	gcc				2112
ctg Leu 705	gat	acg Thr	agc Ser	aac Asn	tcc Ser 710	agc	gac Asp	gaa Glu	gcc Ala	gtc Val 715	agc Ser	atg Met	agt Ser	aac Asn	acg Thr 720	2160
tct	cca Pro	agc Ser	gag Glu	agc Ser 725	agt	aca Thr	gaa Glu	caa Gln	aaa Lys 730	tcc	aga Arg	cgc Arg	ttc Phe	cag Gln 735	tgc	2208
				tta							agt Ser			aca		2256
											acg Thr					2304
cat His	caa Gln 770	atg	gca Ala	cag Gln	tat Tyr	cgc Arg 775	gaa	atc Ile	gag Glu	cag Gln	atg Met 780	ctg	cta Leu	tcc Ser	aag Lys	2352
tgc		aac	aca	gag	ccg		gag	cag		cag age	agt	gag	gcg	gaa	cgt	2400

						G	NCA-	P03-	·007s	Seane	ncel	isti	na t	-xt		
Cys 785	Ala	Asn	Thr	Glu	Pro 790	Pro	Glu	Gln	Glu	Gln 795	Ser	Glu	Ala	Ğlu	Arg 800	
ttt Phe	agt Ser	gcc Ala	tgc Cys	ctg Leu 805	gcc Ala	gca Ala	tac Tyr	cga Arg	ccc Pro 810	aag Lys	ccg Pro	cac His	ctg Leu	cta Leu 815	aca Thr	2448
	gcc Ala													Lys		2496
tgc Cys	gcc Ala	cga Arg 835	ctg Leu	cca Pro	agc Ser	gac Asp	acg Thr 840	ttc	acc Thr	aag Lys	ttg Leu	acg Thr 845	gcg Ala	ttg Leu	tgg Trp	2544
cgc Arg	tgc Cys 850	acc Thr	cga Arg	aac Asn	gaa Glu	agg Arg 855	gct Ala	gga Gly	gtg Val	acc Thr	ctg Leu 860	ttt Phe	cag Gln	tac Tyr	aca Thr	2592
ctc Leu 865	cgt Arg	ctg Leu	ccc Pro	atc Ile	aac Asn 870	tcg Ser	cca Pro	ttg Leu	aag Lys	cat His 875	gac Asp	att Ile	gtg Val	ggt Gly	ctt Leu 880	2640
ccg Pro	atg Met	cca Pro	act Thr	caa Gln 885	aca Thr	ttg Leu	gcc Ala	cgc Arg	cga Arg 890	ctg Leu	gct Ala	gcc Ala	ttg Leu	cag Gln 895	Ala	2688
tgc Cys	gtg Val	gaa Glu	ctg Leu 900	cac His	agg Arg	atc Ile	ggt Gly	gag Glu 905	tta Leu	gac Asp	gat Asp	cag Gln	ttg Leu 910	cag Gln	cct Pro	2736
atc Ile	ggc Gly	aag Lys 915	gag Glu	gga Gly	ttt Phe	cgt Arg	gcc Ala 920	ctg Leu	gag Glu	ccg Pro	gac Asp	tgg Trp 925	gag Glu	tgc Cys	ttt Phe	2784
gaa Glu	ctg Leu 930	gag Glu	cca Pro	gag Glu	gac Asp	gaa Glu 935	cag Gln	att Ile	gtg Val	cag Gln	cta Leu 940	agc Ser	gat Asp	gaa Glu	cca Pro	2832
cgt Arg 945	ccg Pro	gga Gly	aca Thr	acg Thr	aag Lys 950	cgt Arg	cgt Arg	cag Gln	tac Tyr	tat Tyr 955	tac Tyr	aaa Lys	cgc Arg	att Ile	gca Ala 960	2880
tcc Ser	gaa Glu	ttt Phe	tgc Cys	gat Asp 965	tgc Cys	cgt Arg	ccc Pro	gtt Val	gcc Ala 970	gga Gly	gcg Ala	cca Pro	tgc Cys	tat Tyr 975	ttg Leu	2928
tac Tyr	ttt Phe	atc Ile	caa Gln 980	ctg Leu	acg Thr	ctc Leu	caa Gln	tgt Cys 985	ccg Pro	att Ile	ccc Pro	gaa Glu	gag Glu 990	caa Gln	aac Asn	2976
								Pro					n G		ga ttc ly Phe	3024
	att Ile 1010	Lei	a aco ı Thr	aco Thr	aaa Lys	cgg Arg 102	] I	ta co le P	cc aa ro L	ag ci	eu S	gt er 020	gct Ala			3069
	ttc Phe 1025	Thr			ggt		ı Va	tg aa al L	ag g ys Va	tt to al So	er L	tg eu 035	gag Glu	tta Leu	gct Ala	3114
	gaa Glu 1040	Arç			cta Lei		^ S		aa ca lu G		le v	tc al 050	tgc Cys			3159
	ttt Phe 1055	Lei			acg Thr		e Tl				eŭ A		ttg Leu			3204
	ctg Leu 1070	Met			gat Asp		) A:		cc a er T		aa a lu A	at '	tgt Cys			3249
	gtg Val 1085	Pro			aag Lys		a P		ct g la G		gc a	ag	cac His			3294
	cag Gln 1100	ttt Phe			g ctg Lei	ato	c c		cg a		ga a ly A	at .	aca Thr			3339
cgg	gca		g cco	ga1	gag			gc c	ag g	cg ca Page	ag c		ttt	gat	ccg	3384

Arg   Ala   Val   Pro   Asp   Glu   Arg   Gln   Ala   Gln   Pro   Phe   Asp   Pro   Arg   Gln   Ala   Gln   Pro   Phe   Asp   Asp   Ala   Val   Val   Met   Pro   Trp   Tyr   Arg   Ash   Gln   Asp   Ala   Val   Val   Met   Pro   Trp   Tyr   Arg   Ash   Gln   Asp   Ala   Val   Val   Ala   Glu   Tle   Cys							GNC	Δ – ΡΛ	3-00	75aa	Henc	el ist	ina	tvt		
Simple   Pro   Simple   Simp	Arg						Glu 1120	Arg	Gln	Ala	Gln	Pro			Pro	
gat caa caa caa caa caa caa caa caa caa c		Arg					Val					Tyr	_		_ ~	3429
See		Gln					Tyr					Cys				3474
Cac		cca Pro					cct Pro	ggt Gly				cgc Arg			_	3519
cag ccg cdg cleu Leu Asp Val A		tac Tyr					tat Tyr					cag Gln			_	3564
Cace		ccg Pro					gat Asp					cgg Arg				3609
agt tcg         gag gag gag aca aag         cgg         gca aag         cgc gag gag         ctc gal cag         ctc tgc act gtg         cca tcc cat tc cca         3744           Lys Gln         1225         ttg tgg cga act gcc         gcc         cca tgg cct         ccc tgc         cca tcc tgc         3748           Ala Ser         ttg tgg cga act gcc         gcc         gcc         ccc tgc         ctc tgc         sac ggt tct gcc         ccc tgc         sac ggt tct gcc         sac ggt tct gcc         sac ggt tct gcc         ccc tgc         sac ggt tct gcc         sac ggt gat gac gac gac gat gac gac gac gac gat gac		acg Thr					aat Asn					gct Ala				3654
aag cag         Lys Gln         Ile Leu Val Pro Glu         Leu Cys Thr Val His 1245         cca ttc ccc         3744           Lys Gln         Ile Leu Val Pro Glu         Leu Cys Thr Val His 1245         Pro Phe Pro Pro Phe Pro 1246         3789           gcc tcc ttg ttg tgg cga act gg gg cgg act ctg ccc ttg tal 1250         240         1245         atc ctg tac atc ctg tac atc ctg tac atc ctg tac atc cgg acg atc gar		tcg Ser					cgg Arg					aat Asn				3699
Sec		cag Gln					gag Glu					cat His				3744
Cgc   ata   Ash   Gly   Leu		tcc Ser					gcc Ala					tgc Cys				3789
Ser Ala		ata Ile					ttg Leu					cgg Arg				3834
ttc gag       tgg       ccc atg       ctg       gac       ttt ggg       tgg       ctc atg       ser Glu       val         1295       aaa       tcg       cgg       gag       tcc       aaa       caa       aag       ggg       gt       ctt agg       ggg       gat       ctt agg       ggg       gat       gat <td></td> <td>gcg Ala</td> <td></td> <td></td> <td></td> <td></td> <td>gga Gly</td> <td></td> <td></td> <td></td> <td></td> <td>gaa Glu</td> <td></td> <td></td> <td></td> <td>3879</td>		gcg Ala					gga Gly					gaa Glu				3879
ctc aag aaa tcg cgg gag tcc Lys Ser Arg Glu Ser 1310 gat act att aat ggc aaa gac tta agt agt act agg gag gag acc caa cta Asp Thr 11e Asn Gly Lys Asp 1330 act agc gag gag acc caa cta 3340 gtt gag aaa agt gct att gaa Asp Lys Asp Lys Asp Lys Asp 1340 gtt gag aaa agt gct att gaa Asp Lys Asp Asp Lys Asp Asp Lys Asp Lys Asp Asp Lys Asp Lys Asp Asp Asp Lys Asp Asp Asp Lys Asp Asp Lys Asp Asp Lys Asp Asp Asp Lys Asp Asp Asp Lys Asp Asp Asp Lys 1365 ctg caa gag gct gat gac ttc Leu Ile Ile Glu Ile Gly Ile Gly Thr Trp Ser Asn 1370 gat atg gc gac gat ata gct Ala Asp Asp Ile Ala Asp Asp Met Ala Asp Asp Ile Ala Asp Asp Ile Ala Asp Asp Ala Phe His Leu 1405 gag gat gac gac caa acg cgc ttc cat ctc Cat ctc Asp Asp Asp Ala Phe His Leu 1405 ttc tgt gat cag caa acg cgc ttc aac ggt tcg ccc aca acg agc agc agc Asp Gln Gln Thr Arg 1415 gtg agc act act agg gag gat cca acg cag acg acg acg acg acg acg acg		gag Glu					gac Asp	ttt Phe	ggg Gly	tgg Trp	agt Ser	cta Leu				3924
gat act       att aat ggc aaa gac       tta gct gat gtt gaa       aag aaa ccg       4014         Asp Thr 1325       Ile Asn Gly Lys Asp 1330       Leu Ala Asp Val Glu Lys Lys Lys Pro 1335       Leu Ala Asp Val Glu Lys Lys Lys Pro 1335       Leu Ala Asp Val Glu Lys Lys Lys Pro 1335       Leu Ala Asp Val Glu Lys Lys Lys Lys Pro 1335       Leu Ala Asp Val Glu Lys		aag Lys					tcc Ser	aaa Lys	caa Gln	aag Lys	gag Glu	tcc Ser		_	_	3969
act agc gag gag acc caa cta gat aag gat tca aaa gac gat aag 4059 Thr Ser Glu Glu Thr Gln Leu 1345 gtt gag aaa agt gct att gaa cta att gag gag gag gag gag gag gag gag g	_	act Thr					gac Asp	tta Leu	gct Ala	gat Asp	gtt Val	gaa Glu				4014
gtt gag aaa agt gct att gaa cta atc att gag gga gag gag aag 4104 Val Glu Lys Ser Ala Ile Glu Leu Ile Ile Glu Gly 1365 Ctg caa gag gct gat gac ttc att gag ata ggc act tgg tca aac 4149 Leu Gln Glu Ala Asp Asp Phe 1375 gat atg gcc gac gat ata gct agt ttt aac caa gaa gac gac gac 4194 Asp Met Ala Asp Asp Ile Ala Ser Phe Asn Gln Glu Asp Asp Asp 1385 gag gat gac gcc ttc cat ctc cca gtt tta ccg gca aac gtt aag 4239 Glu Asp Asp Ala Phe His Leu Pro Ala Asp Asp Cln Gln Thr Arg 1400 ttc tgt gat cag caa acg cgc ttc acg gtt tcg ccc aca ttt tgg gat 4284 Phe Cys Asp Gln Gln Thr Arg 1420 gtg agc aat ggc gaa agc ggc ttc aag ggt cca aag agc agc agc 4329 gtg agc acg aat ggc gac acg acg acg gac 4194 Tyr Gly Ser Pro Thr Phe Trp Asp 1425 gtg agc aat ggc gaa agc ggc ttc aag ggt cca aag agc agt cag 4329		agc Ser					cta Leu	_	-	_		aaa Lys				4059
ctg caagag gct gat gacttcatt gag ata ggc act tgg tca aac4149Leu GlnGlu Ala Asp Asp Asp Phe 137013751380Trp Ser Asngat atggcc gac gat ata gct Asp Met 1385agt ttt aac caa gaa 1390gac gac gac gac 13904194Asp Met 1385Ala Asp Asp Ile Ala 1390Ser Phe Asn Gln Glu 1390Asp Asp Asp Asp Asp 1395Asp Asp Asp Asp 14004239Glu Asp 1400Asp Asp Ala Phe His 1400Leu 1405Pro Val Leu Pro Ala 1410Asn Val Lys 14104284Ttc tgt 1420gat cag caa acg cgc 1420tac ggt tcg ccc aca 1420ttt tgg gat 14254284gtg agcaat ggc gaa agc ggcttc aag ggt cca aag 1420agc agt cag4329		gag Glu					gaa Glu					gga Gly				4104
gat atg gcc gac gat ata gct agt ttt aac caa gaa gac gac gac 4194  Asp Met Ala Asp Asp Ile Ala Ser Phe Asn Gln Glu Asp Asp Asp 1395  gag gat gac gcc ttc cat ctc cca gtt tta ccg gca aac gtt aag Glu Asp Asp Ala Phe His Leu Pro Val Leu Pro Ala Asn Val Lys 1400  ttc tgt gat cag caa acg cgc tac ggt tcg ccc aca ttt tgg gat Phe Cys Asp Gln Gln Thr Arg Tyr Gly Ser Pro Thr Phe Trp Asp 1415 gtg agc aat ggc gaa agc ggc ttc aag ggt cca aag agc agt cag  4194  4239  4239  4284  Asp		caa Gln					ttc Phe					act Thr				4149
gag gat gac gcc ttc cat ctc cca gtt tta ccg gca aac gtt aag Glu Asp Asp Ala Phe His Leu Pro Val Leu Pro Ala Asn Val Lys 1400 1405 1410  ttc tgt gat cag caa acg cgc tac ggt tcg ccc aca ttt tgg gat 4284 Phe Cys Asp Gln Gln Thr Arg Tyr Gly Ser Pro Thr Phe Trp Asp 1415 1420 1425 gtg agc aat ggc gaa agc ggc ttc aag ggt cca aag agc agt cag 4329	-	atg Met	gcc Ala	gac Asp	gat Asp	ata Ile	gct Ala					gaa Glu	_	-	_	4194
ttc tgt gat cag caa acg cgc tac ggt tcg ccc aca ttt tgg gat Phe Cys Asp Gln Gln Thr Arg Tyr Gly Ser Pro Thr Phe Trp Asp 1415 1420 1425 gtg agc aat ggc gaa agc ggc ttc aag ggt cca aag agc agt cag 4329		gat Asp					ctc Leu					gca Ala				4239
gtg agc aat ggc gaa agc ggc ttc aag ggt cca aag agc agt cag 4329		tgt Cys					cgc Arg					aca Thr				4284
	gtg		aat	ggc	gaa	agc	_	ttc	aag			aag	agc	agt	cag	4329

						GNC	A-P0	3-00	7Seq	uenc	eList	ing.	txt		
٧a٦	Ser 1430	Asn	Gly	Glu	Ser								Ser	Gln	
	aag Lys 1445	cag Gln	ggt Gly	ggc Gly	aag Lys	ggc Gly 1450	aaa Lys	gca Ala	aag Lys	ggt Gly	ccg Pro 1455	~ -	aag Lys	_	4374
	ttt Phe 1460			tat Tyr	_	tcg ser 1465					ggt Gly 1470		agc Ser		4419
	gac Asp 1475			aac Asn			_	ctc Leu			_		cac His		4464
	agt Ser 1490			gac Asp				gca Ala			atc Ile 1500	gat Asp	gcg Ala	gga Gly	4509
	att Ile 1505			acc Thr		aag Lys 1510					act Thr 1515		gaa Glu		4554
	cag Gln 1520	gaa Glu	gtg Val	gaa Glu	aag Lys	cgc Arg 1525		aag Lys			tcc Ser 1530		atc Ile		4599
	acc Thr 1535	aat Asn	gct Ala	aac Asn	gag Glu	cgg Arg 1540		tat Tyr					aac Asn		4644
ctc Leu	att Ile 1550			aat Asn			cat His	gag Glu	gac Asp	cag Gln	aag Lys 1560		cct Pro		4689
	ata Ile 1565			gaa Glu				gct Ala					gaa Glu		4734
gaa Glu	tcc Ser 1580			atg Met				cac His				_	gtt Val		4779
	aga Arg 1595			gcc Ala				cag Gln			aag Lys 1605		tcg Ser		4824
atg Met	gag Glu 1610			aag Lys				ccg Pro					gat Asp		4869
	gcc Ala 1625			ctg Leu				cgc Arg			ctg Leu 1635		tcg Ser		4914
	gta Val 1640			aat Asn		gat Asp 1645		gta Val			cat His 1650		cag Gln		4959
	tac Tyr 1655	aat Asn	gta Val	atg Met	gga Gly	tgc Cys 1660	gga Gly	gat Asp	agt Ser	ttt Phe	gac Asp 1665		tat Tyr		5004
gat Asp				ctg Leu				gaa Glu					ctg Leu		5049
	gaa Glu 1685	cga Arg	att Ile	gaa Glu	att Ile	gag Glu 1690		cct Pro			acg Thr 1695		gcc Ala		5094
	tca Ser 1700			tta Leu				ttc Phe			gat Asp 1710	_	caa Gln	-	5139
-	cta Leu 1715	gtg Val	ggc Gly	cat His	cca Pro	gga Gly 1720		agt Ser			atc Ile 1725	att Ile	ttg Leu	caa Gln	5184
	ctc Leu 1730			tcc Ser				gat Asp					gag Glu		5229
ctg	gag	aca	att	gga	gat	-	ttt	cta		tat e 18	gcc	att	acc	acc	5274

LAU	clu	The	Tlo	cly	A c n						eList			The	
	1745			•	•	Ser 1750			-	•	Ala 1755		Thr		5210
	ttg Leu 1760	Tyr	Ile	Thr	Tyr	gag Glu 1765	aat Asn	ya l	His	gag Glu	gga Gly 1770		Leu		5319
	ctg Leu 1775	cgc Arg	tcc Ser	aag Lys	cag Gln	gtt Val 1780	gcc Ala	aat Asn	ctc Leu	aat Asn	ctc Leu 1785	tat Tyr	cgt Arg	ctg Leu	5364
	aga Arg 1790			aga Arg				tat Tyr					aaa Lys		5409
	ccg Pro 1805		_	aat Asn				ccc Pro					cca Pro	_	5454
	cta Leu 1820	gag Glu	aag Lys	gcg Ala	ctc Leu	atc Ile 1825		gcg Ala	aag Lys	atc Ile	CCC Pro		cac His		5499
	aag Lys 1835					cta Leu 1840					Leu		agt Ser		5544
	atc Ile 1850					cgc Arg		aaa Lys			Āla		ggc Gly		5589
	cag Gln 1865					1855 caa Gln 1870		gga Gly			Asp	_	tcc Ser		5634
-	agc Ser 1880					agc Ser		ttt Phe					ctt Leu		5679
	caa Gln 1895			att Ile		1885 gat Asp 1900		tct Ser			1890 gat Asp 1905		gtc Val		5724
	ctc Leu 1910			gcc Ala		ctc	att Ile	gag Glu	tgc Cys	gga Gly	CCC		ggg Gly		5769
	ctc Leu 1925	ttt Phe	atg Met	gcc Ala	tgg Trp	ctg	ggc Gly	gtg Val	aga Arg	gtg Val			atc Ile		5814
	cag Gln 1940	ttg Leu	gac Asp	ggg Gly	ggt Gly	aac Asn 1945	cag Gln	gag Glu	caa Gln	cga Arg			ggt Gly		5859
	aaa Lys 1955	ccg Pro	aat Asn	gcc Ala	gaa Glu	aat	gtg Val	gtc Val	acc Thr	gtt Val			gca Ala		5904
	acg Thr 1970										cca		gct Ala		5949
gag Glu	gag Glu 1985			cag Gln		cta	agc Ser	ggc Gly	ttt Phe	gag Glu	gag		gag Glu		5994
agt Ser				aag Lys				cgg Arg			ctg		caa Gln		6039
	aca Thr 2015			agt Ser				aat Asn			-		tgc Cys		6084
cag Gln	cgt Arg 2030	ctg Leu	gag Glu	ttc Phe	ctg Leu		gat Asp	gct Ala	gtt Val	cta Leu	gat	tac Tyr	ctc Leu		6129
	cgg Arg 2045			tac Tyr		gat							ggc Gly		6174
tta	acg	gat	ttg	cgg	tca		ctg	gtg		aat e 19	aca	ata	ttc	gcc	6219

evie :

```
GNCA-P03-007SequenceListing.txt
          Asp Leu Arg Ser Ala Leu Val Asn Asn Thr Ile Phe Ala
Leu Thr
     2060
                               2065
                                                         2070
tcc ctg gct gtt cgc cat ggc ttc cac aag ttc ttc cgg cac ctc
Ser Leu Ala Val Arg His Gly Phe His Lys Phe Phe Arg His Leu
                                                                                     6264
                               2080
     2075
                                                         2085
          ggc ctt aac gat gtg att gac cgt ttt gtg
                                                                                     6309
tcg ccg
                                                               cgg atc cag
          Gly Leu Asn Asp Val
                                     Ile Asp Arg Phe Val
Ser Pro
                                                               Arg Ile Gln
     2090
                               2095
                                                         2100
                                     agt gag gag tac tac
Ser Glu Glu Tyr Tyr
cag gag
          aat gga cac tgc atc
                                                               tta ttg tcc
                                                                                     6354
Gln Glu
          Asn Gly His Cys Ile
                                                               Leu Leu Ser
     2105
                               2110
                                                         2115
           gag tgc gat gac gcc
                                     gag gac gtt gag gtg
                                                                                     6399
gag gag
                                                               ccc aag gca
Glu Glu
           Glu Cys Asp Asp Ala
                                     Glu Asp Val Glu Val
                                                               Pro Lys Ala
     2120
                               2125
                                                         2130
          gac gtt ttc gag tcg
Asp Val Phe Glu Ser
                                     atc gca ggt gcc att
Ile Ala Gly Ala Ile
                                                                                     6444
ttg ggc
                                                               ttt ctc gac
    Ğly
                                                               Phe Leu Asp
                               2140
     2135
                                                         2145
          atg tcg ctg gac gtg
                                     gtt tgg cac gta tat
Val Trp His Val Tyr
                                                                                     6489
tca aac
                                                               agc aac atg
Ser Asn
          Met Ser Leu Asp Val
                                                               Ser Asn Met
     2150
                               2155
                                                         2160
atg agc
           ccg gag atc gag cag
                                     ttc agc aac tca gtg
                                                                                     6534
                                                               cca aaa tcg
Met Ser
          Pro Glu Ile Glu Gln
                                     Phe Ser Asn Ser Val
                                                               Pro Lys Ser
     2165
                               2170
                                                         2175
          cgg gag ctc ctc gag
Arg Glu Leu Leu Glu
                                    ctg gag ccg gaa acc
Leu Glu Pro Glu Thr
ccc att
                                                               gcc aag ttc
                                                                                     6579
Pro Ile
                                                               Ala Lys Phe
     2180
                               2185
                                                         2190
           ccc gag aag ctg gcg
Pro Glu Lys Leu Ala
                                     gat ggg cga cgg gtg
Asp Gly Arg Arg Val
ggc aag
                                                               cgc gtt acc
                                                                                     6624
Gly Lys
                                                               Arg Val Thr
     2195
                               2200
                                                         2205
          gtc ttc tgc aaa gga acc ttc cgt ggc atc
Val Phe Cys Lys Gly Thr Phe Arg Gly Ile
gtg gat
                                                               gga cgc aac
                                                                                     6669
Val Asp
                                                               Gly Arg Asn
     2210
                               2215
                                                         2220
tat cgc att gcc aag tgc acg gcg gcc aaa tgc gca ttg cgc caa
Tyr Arg Ile Ala Lys Cys Thr Ala Ala Lys Cys Ala Leu Arg Gln
                                                                                     6714
                               2230
     2225
                                                         2235
ctc aaa aag cag ggc ttg ata gcc aaa aaa gac taa
Leu Lys Lys Gln Gly Leu Ile Ala Lys Lys Asp
                                                                                     6750
     2240
                               2245
<210>
<211>
        2249
<212>
        PRT
        Drosophila melanogaster
<213>
<400>
Met Ala Phe His Trp Cys Asp Asn Asn Leu His Thr Thr Val Phe Thr
Pro Arg Asp Phe Gln Val Glu Leu Leu Ala Thr Ala Tyr Glu Arg Asn 20 25 30
Thr Ile Ile Cys Leu Gly His Arg Ser Ser Lys Glu Phe Ile Ala Leu \frac{1}{35}
Lys Leu Leu Gln Glu Leu Ser Arg Arg Ala Arg Arg His Gly Arg Val
Ser Val Tyr Leu Ser Cys Glu Val Gly Thr Ser Thr Glu Pro Cys Ser
65 70 75 80
Ile Tyr Thr Met Leu Thr His Leu Thr Asp Leu Arg Val Trp Gln Glu
                                             90
```

GNCA-P03-007SequenceListing.txt Gln Pro Asp Met Gln Ile Pro Phe Asp His Cys Trp Thr Asp Tyr His 100 105 110 Val Ser Ile Leu Arg Pro Glu Gly Phe Leu Tyr Leu Leu Glu Thr Arg 115 120 125 Glu Leu Leu Ser Ser Val Glu Leu Ile Val Leu Glu Asp Cys His 130 135 140 Asp Ser Ala Val Tyr Gln Arg Ile Arg Pro Leu Phe Glu Asn His Ile 145 150 155 160 Met Pro Ala Pro Pro Ala Asp Arg Pro Arg Ile Leu Gly Leu Ala Gly 165 170 175 Pro Leu His Ser Ala Gly Cys Glu Leu Gln Gln Leu Ser Ala Met Leu 180 185 190 Ala Thr Leu Glu Gln Ser Val Leu Cys Gln Ile Glu Thr Ala Ser Asp 195 200 205 Ile Val Thr Val Leu Arg Tyr Cys Ser Arg Pro His Glu Tyr Ile Val 210 215 220 Gln Cys Ala Pro Phe Glu Met Asp Glu Leu Ser Leu Val Leu Ala Asp 225 230 235 240 Val Leu Asn Thr His Lys Ser Phe Leu Leu Asp His Arg Tyr Asp Pro 245 250 255 Tyr Glu Ile Tyr Gly Thr Asp Gln Phe Met Asp Glu Leu Lys Asp Ile 260 265 270 Pro Asp Pro Lys Val Asp Pro Leu Asn Val Ile Asn Ser Leu Leu Val 275 280 285 Val Leu His Glu Met Gly Pro Trp Cys Thr Gln Arg Ala Ala His His 290 295 300 Phe Tyr Gln Cys Asn Glu Lys Leu Lys Val Lys Thr Pro His Glu Arg 305 310 315 320 His Tyr Leu Leu Tyr Cys Leu Val Ser Thr Ala Leu Ile Gln Leu Tyr 325 330 335 Ser Leu Cys Glu His Ala Phe His Arg His Leu Gly Ser Gly Ser Asp 340 350 Ser Arg Gln Thr Ile Glu Arg Tyr Ser Ser Pro Lys Val Arg Arg Leu 355 360 365 Leu Gln Thr Leu Arg Cys Phe Lys Pro Glu Glu Val His Thr Gln Ala 370 380 Asp Gly Leu Arg Arg Met Arg His Gln Val Asp Gln Ala Asp Phe Asn 385 390 395 Arg Leu Ser His Thr Leu Glu Ser Lys Cys Arg Met Val Asp Gln Met 405 410 415 Asp Gln Pro Pro Thr Glu Thr Arg Ala Leu Val Ala Thr Leu Glu Gln 420 430

GNCA-P03-007SequenceListing.txt

Ile Leu His Thr Thr Glu Asp Arg Gln Thr Asn Arg Ser Ala Ala Arg
435
440
445 Val Thr Pro Thr Pro Thr Pro Ala His Ala Lys Pro Lys Pro Ser Ser 450 455 460 Gly Ala Asn Thr Ala Gln Pro Arg Thr Arg Arg Arg Val Tyr Thr Arg 465 470 475 480Arg His His Arg Asp His Asn Asp Gly Ser Asp Thr Leu Cys Ala Leu 485 490 495 Ile Tyr Cys Asn Gln Asn His Thr Ala Arg Val Leu Phe Glu Leu Leu 500 510 Ala Glu Ile Ser Arg Arg Asp Pro Asp Leu Lys Phe Leu Arg Cys Gln 515 520 525 Tyr Thr Thr Asp Arg Val Ala Asp Pro Thr Thr Glu Pro Lys Glu Ala 530 540 Glu Leu Glu His Arg Arg Gln Glu Glu Val Leu Lys Arg Phe Arg Met 545 550 555 560 His Asp Cys Asn Val Leu Ile Gly Thr Ser Val Leu Glu Glu Gly Ile 565 570 575 Asp Val Pro Lys Cys Asn Leu Val Val Arg Trp Asp Pro Pro Thr Thr 580 585 590 Tyr Arg Ser Tyr Val Gln Cys Lys Gly Arg Ala Arg Ala Ala Pro Ala 595 600 605 Tyr His Val Ile Leu Val Ala Pro Ser Tyr Lys Ser Pro Thr Val Gly 610 620 Ser Val Gln Leu Thr Asp Arg Ser His Arg Tyr Ile Cys Ala Thr Gly 625 630 635 640 Asp Thr Thr Glu Ala Asp Ser Asp Ser Asp Ser Ala Met Pro Asn 645 650 655 Ser Ser Gly Ser Asp Pro Tyr Thr Phe Gly Thr Ala Arg Gly Thr Val 660 665 670 Lys Ile Leu Asn Pro Glu Val Phe Ser Lys Gln Pro Pro Thr Ala Cys 675 680 685 Asp Ile Lys Leu Gln Glu Ile Gln Asp Glu Leu Pro Ala Ala Ala Gln 690 695 700 Leu Asp Thr Ser Asn Ser Ser Asp Glu Ala Val Ser Met Ser Asn Thr 705 710 715 720Ser Pro Ser Glu Ser Ser Thr Glu Gln Lys Ser Arg Arg Phe Gln Cys 725 730 735 Glu Leu Ser Ser Leu Thr Glu Pro Glu Asp Thr Ser Asp Thr Thr Ala 740 745 750 Glu Ile Asp Thr Ala His Ser Leu Ala Ser Thr Thr Lys Asp Leu Val 755 760 765

GNCA-P03-007SequenceListing.txt
His Gln Met Ala Gln Tyr Arg Glu Ile Glu Gln Met Leu Leu Ser Lys
770 780 Cys Ala Asn Thr Glu Pro Pro Glu Gln Glu Gln Ser Glu Ala Glu Arg 785 790 795 800 Phe Ser Ala Cys Leu Ala Ala Tyr Arg Pro Lys Pro His Leu Leu Thr 805 810 815 Gly Ala Ser Val Asp Leu Gly Ser Ala Ile Ala Leu Val Asn Lys Tyr 820 825 830 Cys Ala Arg Leu Pro Ser Asp Thr Phe Thr Lys Leu Thr Ala Leu Trp 835 840 845 Arg Cys Thr Arg Asn Glu Arg Ala Gly Val Thr Leu Phe Gln Tyr Thr 850 855 860 Leu Arg Leu Pro Ile Asn Ser Pro Leu Lys His Asp Ile Val Gly Leu 865 870 875 880 Pro Met Pro Thr Gln Thr Leu Ala Arg Arg Leu Ala Ala Leu Gln Ala 885 890 895 Cys Val Glu Leu His Arg Ile Gly Glu Leu Asp Asp Gln Leu Gln Pro 900 905 910 Ile Gly Lys Glu Gly Phe Arg Ala Leu Glu Pro Asp Trp Glu Cys Phe 915 925 Glu Leu Glu Pro Glu Asp Glu Gln Ile Val Gln Leu Ser Asp Glu Pro 930 935 940 Arg Pro Gly Thr Thr Lys Arg Arg Gln Tyr Tyr Tyr Lys Arg Ile Ala 945 950 955 960 Ser Glu Phe Cys Asp Cys Arg Pro Val Ala Gly Ala Pro Cys Tyr Leu 965 970 975 Tyr Phe Ile Gln Leu Thr Leu Gln Cys Pro Ile Pro Glu Glu Gln Asn 980 985 990 Thr Arg Gly Arg Lys Ile Tyr Pro Pro Glu Asp Ala Gln Gln Gly Phe 995 1000 1005 Gly Ile Leu Thr Thr Lys Arg Ile Pro Lys Leu Ser Ala Phe Ser 1010 1015 1020 Ile Phe Thr Arg Ser Gly Glu Val Lys Val Ser Leu Glu Leu Ala 1025 1030 1035 Lys Glu Arg Val Ile Leu Thr Ser Glu Gln Ile Val Cys Ile Asn 1050 1045 1040 Gly Phe Leu Asn Tyr Thr Phe Thr Asn Val Leu Arg Leu Gln Lys 1060 1055 Phe Leu Met Leu Phe Asp Pro Asp Ser Thr Glu Asn Cys Val Phe 1070 1080 Ile Val Pro Thr Val Lys Ala Pro Ala Gly Gly Lys His Ile Asp 1085 1090 1095 1090 1085

GNCA-P03-007SequenceListing.txt Trp Gln Phe Leu Glu Leu Ile Gln Ala Asn Gly Asn Thr Met Pro 1100 1105 1110 Arg Ala Val Pro Asp Glu Glu Arg Gln Ala Gln Pro Phe Asp Pro Gln Arg Phe Gln Asp Ala Val Val Met Pro Trp Tyr Arg Asn Gln 1130 1135 1140 Asp Gln Pro Gln Tyr Phe Tyr Val Ala Glu Ile Cys Pro His Leu 1145 1150 Ser Pro Leu Ser Cys Phe Pro Gly Asp Asn Tyr Arg Thr Phe Lys 1160 1165 1170 1160 His Tyr Tyr Leu Val Lys Tyr Gly Leu Thr Ile Gln Asn Thr Ser 1175 1180 1185 Gln Pro Leu Leu Asp Val Asp His Thr Ser Ala Arg Leu Asn Phe 1190 1195 1200 1190 Leu Thr Pro Arg Tyr Val Asn Arg Lys Gly Val Ala Leu Pro Thr Ser Ser Glu Glu Thr Lys Arg Ala Lys Arg Glu Asn Leu Glu Gln 1220 1230 1220 Lys Gln Ile Leu Val Pro Glu Leu Cys Thr Val His Pro Phe Pro Ala Ser Leu Trp Arg Thr Ala Val Cys Leu Pro Cys Ile Leu Tyr 1250 1255 1260 Arg Ile Asn Gly Leu Leu Leu Ala Asp Asp Ile Arg Lys Gln Val 1265 1270 1275 Ser Ala Asp Leu Gly Leu Gly Arg Gln Gln Ile Glu Asp Glu Asp 1280 1285 Phe Glu Trp Pro Met Leu Asp Phe Gly Trp Ser Leu Ser Glu Val Leu Lys Lys Ser Arg Glu Ser Lys Gln Lys Glu Ser Leu Lys Asp 1310 1315 1320 Asp Thr Ile Asn Gly Lys Asp Leu Ala Asp Val Glu Lys Lys Pro 1325 1330 1335 Thr Ser Glu Glu Thr Gln Leu Asp Lys Asp Ser Lys Asp Asp Lys 1340 1345 1350 Val Glu Lys Ser Ala Ile Glu Leu Ile Ile Glu Gly Glu Glu Lys 1355 1360 1365 1360 Leu Gln Glu Ala Asp Asp Phe Ile Glu Ile Gly Thr Trp Ser Asn 1380 Asp Met Ala Asp Asp Ile Ala Ser Phe Asn Gln Glu Asp Asp Asp 1385 1390 1395 Glu Asp Asp Ala Phe His Leu Pro Val Leu Pro Ala Asn Val Lys 1405

GNCA-P03-007SequenceListing.txt Phe Cys Asp Gln Gln Thr Arg Tyr Gly Ser Pro Thr Phe Trp Asp 1415 1420 1425 Val Ser Asn Gly Glu Ser Gly Phe Lys Gly Pro Lys Ser Ser Gln 1430 1435 1440 Asn Lys Gln Gly Gly Lys Gly Lys Ala Lys Gly Pro Ala Lys Pro 1445 1450 Thr Phe Asn Tyr Tyr Asp Ser Asp Asn Ser Leu Gly Ser Ser Tyr 1460 1470 Asp Asp Asp Asp Asn Ala Gly Pro Leu Asn Tyr Met His His Asn 1475 1480 1485 Tyr Ser Ser Asp Asp Asp Val Ala Asp Asp Ile Asp Ala Gly 1490 1495 Arg Ile Ala Phe Thr Ser Lys Asn Glu Ala Glu Thr Ile Glu Thr 1505 1515 Ala Gln Glu Val Glu Lys Arg Gln Lys Gln Leu Ser Ile Ile Gln 1520 1530 1530 Ala Thr Asn Ala Asn Glu Arg Gln Tyr Gln Gln Thr Lys Asn Leu 1535 1540 1545 Leu Ile Gly Phe Asn Phe Lys His Glu Asp Gln Lys Glu Pro Ala 1550 1560 Thr Ile Arg Tyr Glu Glu Ser Ile Ala Lys Leu Lys Thr Glu Ile 1565 1570 1575 Glu Ser Gly Gly Met Leu Val Pro His Asp Gln Gln Leu Val Leu 1585 Lys Arg Ser Asp Ala Ala Glu Ala Gln Val Ala Lys Val Ser Met 1595 1600 1605 Met Glu Leu Leu Lys Gln Leu Leu Pro Tyr Val Asn Glu Asp Val 1615 Leu Ala Lys Lys Leu Gly Asp Arg Glu Leu Leu Leu Ser Asp 1625 1630 1635 Leu Val Glu Leu Asn Ala Asp Trp Val Ala Arg His Glu Gln Glu 1640 1650 Thr Tyr Asn Val Met Gly Cys Gly Asp Ser Phe Asp Asn Tyr Asn 1655 1660 1665 Asp His His Arg Leu Asn Leu Asp Glu Lys Gln Leu Lys Leu Gln 1670 1680 Tyr Glu Arg Ile Glu Ile Glu Pro Pro Thr Ser Thr Lys Ala Ile 1690 Thr Ser Ala Ile Leu Pro Ala Gly Phe Ser Phe Asp Arg Gln Pro 1700 1705 1710 Asp Leu Val Gly His Pro Gly Pro Ser Pro Ser Ile Ile Leu Gln 1715 1720

48 A

...

GNCA-P03-007SequenceListing.txt Ala Leu Thr Met Ser Asn Ala Asn Asp Gly Ile Asn Leu Glu Arg Leu Glu Thr Ile Gly Asp Ser Phe Leu Lys Tyr Ala Ile Thr Thr 1745 1750 1755 Tyr Leu Tyr Ile Thr Tyr Glu Asn Val His Glu Gly Lys Leu Ser His Leu Arg Ser Lys Gln Val Ala Asn Leu Asn Leu Tyr Arg Leu 1780 1785 Gly Arg Arg Lys Arg Leu Gly Glu Tyr Met Ile Ala Thr Lys Phe 1790 1800 Glu Pro His Asp Asn Trp Leu Pro Pro Cys Tyr Tyr Val Pro Lys 1805 1810 1815 1810 Glu Leu Glu Lys Ala Leu Ile Glu Ala Lys Ile Pro Thr His His 1820 Trp Lys Leu Ala Asp Leu Leu Asp Ile Lys Asn Leu Ser Ser Val 1840 Gln Ile Cys Glu Met Val Arg Glu Lys Ala Asp Ala Leu Gly Leu 1850 1860 Glu Gln Asn Gly Gly Ala Gln Asn Gly Gln Leu Asp Asp Ser Asn 1865 1870 1875 Asp Ser Cys Asn Asp Phe Ser Cys Phe Ile Pro Tyr Asn Leu Val 1880 1885 Ser Gln His Ser Ile Pro Asp Lys Ser Ile Ala Asp Cys Val Glu 1900 Ala Leu Ile Gly Ala Tyr Leu Ile Glu Cys Gly Pro Arg Gly Ala 1910 1915 Leu Leu Phe Met Ala Trp Leu Gly Val Arg Val Leu Pro Ile Thr 1925 1930 1935 Arg Gln Leu Asp Gly Gly Asn Gln Glu Gln Arg Ile Pro Gly Ser 1940 1945 1950 Thr Lys Pro Asn Ala Glu Asn Val Val Thr Val Tyr Gly Ala Trp 1955 1960 1965 1960 Pro Thr Pro Arg Ser Pro Leu Leu His Phe Ala Pro Asn Ala Thr 1975 Glu Glu Leu Asp Gln Leu Leu Ser Gly Phe Glu Glu Phe Glu Glu 1990 1995 Ser Leu Gly Tyr Lys Phe Arg Asp Arg Ser Tyr Leu Leu Gln Ala 2000 2005 2010 2010 Met Thr His Ala Ser Tyr Thr Pro Asn Arg Leu Thr Asp Cys Tyr 2015 2020 2025 Gln Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Asp Tyr Leu Ile 2030 2040 2030

GNCA-P03-007SequenceListing.txt Thr Arg His Leu Tyr Glu Asp Pro Arg Gln His Ser Pro Gly Ala 2045 2050 2055 Leu Thr Asp Leu Arg Ser Ala Leu Val Asn Asn Thr Ile Phe Ala 2070 Ser Leu Ala Val Arg His Gly Phe His Lys Phe Phe Arg His Leu 2075 2080 2085 Ser Pro Gly Leu Asn Asp Val Ile Asp Arg Phe Val Arg Ile Gln 2090 2095 2100 Gln Glu Asn Gly His Cys Ile Ser Glu Glu Tyr Tyr Leu Leu Ser 2105 2110 2115 Glu Glu Cys Asp Asp Ala Glu Asp Val Glu Val Pro Lys Ala 2120 2125 2130 Leu Gly Asp Val Phe Glu Ser Ile Ala Gly Ala Ile Phe Leu Asp 2135 2140 2145 Ser Asn Met Ser Leu Asp Val Val Trp His Val Tyr Ser Asn Met 2150 2160 Met Ser Pro Glu Ile Glu Gln Phe Ser Asn Ser Val Pro Lys Ser 2165 2170 2175 Pro Ile Arg Glu Leu Leu Glu Leu Glu Pro Glu Thr Ala Lys Phe 2180 Gly Lys Pro Glu Lys Leu Ala Asp Gly Arg Arg Val Arg Val Thr 2195 2200 2205 Val Asp Val Phe Cys Lys Gly Thr Phe Arg Gly Ile Gly Arg Asn 2210 2220 Tyr Arg Ile Ala Lys Cys Thr Ala Ala Lys Cys Ala Leu Arg Gln 2225 2230 2235 Leu Lys Lys Gln Gly Leu Ile Ala Lys Lys Asp 2240 2245 <210> 1145 <211> <212> PRT Drosophila melanogaster <213> Met Gly Lys Lys Asp Lys Asn Lys Lys Gly Gly Gln Asp Ser Ala Ala 1 10 15 Ala Pro Gln Pro Gln Gln Gln Gln Lys Gln Gln Gln Gln Arg Gln Gln 20 25 30 Gln Pro Gln Gln Leu Gln Gln Pro Gln Gln Leu Gln Gln Pro Gln Gln 35 40 45 Leu Gln Gln Pro Gln Gln Gln Gln Gln Gln Pro His Gln Gln Gln 50 55 60 Gln Gln Ser Ser Arg Gln Gln Pro Ser Thr Ser Ser Gly Gly Ser Arg

GNCA-P03-007SequenceListing.txt
Ala Ser Gly Phe Gln Gln Gly Gly Gln Gln Lys Ser Gln Asp Ala
85 90 95 Glu Gly Trp Thr Ala Gln Lys Lys Gln Gly Lys Gln Gln Val Gln Gly 100 105 110 Trp Thr Lys Gln Gly Gln Gln Gly Gly His Gln Gln Gly Arg Gln Gly 115 120 125 Gln Asp Gly Gly Tyr Gln Gln Arg Pro Pro Gly Gln Gln Gln Gly Gly 130 135 140 His Gln Gln Gly Arg Gln Gly Gln Glu Gly Gly Tyr Gln Gln Arg Pro 145 150 155 160 Pro Gly Gln Gln Gly Gly His Gln Gly Arg Gln Gly Gln Glu 165 170 175 Gly Gly Tyr Gln Gln Arg Pro Ser Gly Gln Gln Gln Gly His Gln 180 185 190 Gln Gly Arg Gln Gly Gln Glu Gly Gly Tyr Gln Gln Arg Pro Pro Gly 195 200 205 Gln Gln Gln Gly Gly His Gln Gln Gly Arg Gln Gly Gln Glu Gly Gly 210 215 220 Tyr Gln Gln Arg Pro Ser Gly Gln Gln Gln Gly Gly His Gln Gln Gly 225 230 235 240 Arg Gln Gly Glu Gly Gly Tyr Gln Gln Arg Pro Ser Gly Gln Gln 245 250 255 Gln Gly Gly His Gln Gln Gly Arg Gln Gly Gln Glu Gly Gly Tyr Gln 265 270 Gln Arg Pro Ser Gly Gln Gln Gly Gly His Gln Gln Gly Arg Gln 275 280 285 Gly Gln Glu Gly Gly Tyr Gln Gln Arg Pro Pro Gly Gln Gln Pro Asn 290 295 300 Gln Thr Gln Ser Gln Gly Gln Tyr Gln Ser Arg Gly Pro Pro Gln Gln 305 310 315 320 Gln Gln Ala Ala Pro Leu Pro Leu Pro Pro Gln Pro Ala Gly Ser Ile 325 330 335 Lys Arg Gly Thr Ile Gly Lys Pro Gly Gln Val Gly Ile Asn Tyr Leu 340 350 Asp Leu Asp Leu Ser Lys Met Pro Ser Val Ala Tyr His Tyr Asp Val 355 360 365 Lys Ile Met Pro Glu Arg Pro Lys Lys Phe Tyr Arg Gln Ala Phe Glu 370 375 380 Gln Phe Arg Val Asp Gln Leu Gly Gly Ala Val Leu Ala Tyr Asp Gly 385 390 395 400 Lys Ala Ser Cys Tyr Ser Val Asp Lys Leu Pro Leu Asn Ser Gln Asn 405 410 415 GNCA-P03-007SequenceListing.txt
Pro Glu Val Thr Val Thr Asp Arg Asn Gly Arg Thr Leu Arg Tyr Thr
420 425 430 Ile Glu Ile Lys Glu Thr Gly Asp Ser Thr Ile Asp Leu Lys Ser Leu 435 440 445 Thr Thr Tyr Met Asn Asp Arg Ile Phe Asp Lys Pro Met Arg Ala Met 450 460 Gln Cys Val Glu Val Val Leu Ala Ser Pro Cys His Asn Lys Ala Ile 465 470 475 480 Arg Val Gly Arg Ser Phe Phe Lys Met Ser Asp Pro Asn Asn Arg His 485 490 495 Glu Leu Asp Asp Gly Tyr Glu Ala Leu Val Gly Leu Tyr Gln Ala Phe 500 505 Met Leu Gly Asp Arg Pro Phe Leu Asn Val Asp Ile Ser His Lys Ser 515 520 525 Phe Pro Ile Ser Met Pro Met Ile Glu Tyr Leu Glu Arg Phe Ser Leu 530 540 Lys Ala Lys Ile Asn Asn Thr Thr Asn Leu Asp Tyr Ser Arg Arg Phe 545 550 555 560 Leu Glu Pro Phe Leu Arg Gly Ile Asn Val Val Tyr Thr Pro Pro Gln 565 570 575 Ser Phe Gln Ser Ala Pro Arg Val Tyr Arg Val Asn Gly Leu Ser Arg 580 585 590 Ala Pro Ala Ser Ser Glu Thr Phe Glu His Asp Gly Lys Lys Val Thr 595 600 605 Ile Ala Ser Tyr Phe His Ser Arg Asn Tyr Pro Leu Lys Phe Pro Gln 610 620 Leu His Cys Leu Asn Val Gly Ser Ser Ile Lys Ser Ile Leu Leu Pro 625 630 635 640 Ile Glu Leu Cys Ser Ile Glu Glu Gly Gln Ala Leu Asn Arg Lys Asp 645 650 655 Gly Ala Thr Gln Val Ala Asn Met Ile Lys Tyr Ala Ala Thr Ser Thr 660 665 670 Asn Val Arg Lys Arg Lys Ile Met Asn Leu Leu Gln Tyr Phe Gln His 675 680 685 Asn Leu Asp Pro Thr Ile Ser Arg Phe Gly Ile Arg Ile Ala Asn Asp 690 695 700 Phe Ile Val Val Ser Thr Arg Val Leu Ser Pro Pro Gln Val Glu Tyr 705 710 715 720 His Ser Lys Arg Phe Thr Met Val Lys Asn Gly Ser Trp Arg Met Asp 725 730 735 Gly Met Lys Phe Leu Glu Pro Lys Pro Lys Ala His Lys Cys Ala Val 740 745 750 GNCA-P03-007SequenceListing.txt
Leu Tyr Cys Asp Pro Arg Ser Gly Arg Lys Met Asn Tyr Thr Gln Leu
755 760 765 Asn Asp Phe Gly Asn Leu Ile Ile Ser Gln Gly Lys Ala Val Asn Ile 770 780 Ser Leu Asp Ser Asp Val Thr Tyr Arg Pro Phe Thr Asp Asp Glu Arg 785 790 795 800 Ser Leu Asp Thr Ile Phe Ala Asp Leu Lys Arg Ser Gln His Asp Leu 805 810 815 Ala Ile Val Ile Ile Pro Gln Phe Arg Ile Ser Tyr Asp Thr Ile Lys 820 825 830 Gln Lys Ala Glu Leu Gln His Gly Ile Leu Thr Gln Cys Ile Lys Gln 835 840 845 Phe Thr Val Glu Arg Lys Cys Asn Asn Gln Thr Ile Gly Asn Ile Leu 850 855 860 Leu Lys Ile Asn Ser Lys Leu Asn Gly Ile Asn His Lys Ile Lys Asp 865 870 875 880 Asp Pro Arg Leu Pro Met Met Lys Asn Thr Met Tyr Ile Gly Ala Asp 885 890 895 Val Thr His Pro Ser Pro Asp Gln Arg Glu Ile Pro Ser Val Val Gly 900 905 910 Val Ala Ala Ser His Asp Pro Tyr Gly Ala Ser Tyr Asn Met Gln Tyr 915 920 925 Arg Leu Gln Arg Gly Ala Leu Glu Glu Ile Glu Asp Met Phe Ser Ile 930 940Thr Leu Glu His Leu Arg Val Tyr Lys Glu Tyr Arg Asn Ala Tyr Pro 945 950 955 960 Asp His Ile Ile Tyr Tyr Arg Asp Gly Val Ser Asp Gly Gln Phe Pro 965 970 975 Lys Ile Lys Asn Glu Glu Leu Arg Cys Ile Lys Gln Ala Cys Asp Lys 980 985 990 Val Gly Cys Lys Pro Lys Ile Cys Cys Val Ile Val Val Lys Arg His 995 1000 1005 His Thr Arg Phe Phe Pro Ser Gly Asp Val Thr Thr Ser Asn Lys 1010 1015 1020 Phe Asn Asn Val Asp Pro Gly Thr Val Val Asp Arg Thr Ile Val 1025 1030 1025 His Pro Asn Glu Met Gln Phe Phe Met Val Ser Gly Gln Ala Ile 1040 1045 1050 Gln Gly Thr Ala Lys Pro Thr Arg Tyr Asn Val Ile Glu Asn Thr 1055 1060 1065 Gly Asn Leu Asp Ile Asp Leu Leu Gln Gln Leu Thr Tyr Asn Leu 1075 1070 1080

3 W 1

						_		_							
Cys His 108		Phe	Pro	Arg	GNC Cys 1090	A-PO Asn	3-00 Arg	7Seq Ser	uenc Val	eList Ser 1095	ing. Tyr	txt Pro	Ala		
Pro Ala 110		Leu	Ala	His	Leu 1105	val	Ala	Ala	Arg	Gly 1110	Arg	Val	Tyr		
Leu Thr 111		Thr	Asn	Arg	Phe 1120	Leu	Asp	Leu	Lys	Lys 1125	Glu	Tyr	Ala		
Lys Arg 113		Ile	∨a1	Pro	Glu 1135	Phe	Met	Lys	Lys	Asn 1140	Pro	Met	Tyr		
Phe Val 114															
	6 22 RNA Photi	nus p	oyra]	lis											
<400> ucgaagu	6 acu ca	agcgı	ıaagı	ı ga											22
	7 22 RNA Photi	nus p	oyra:	lis											
<400> uaaagcu	7 uca u	gagud	egcai	ı uc											22
<210> <211> <212> <213>	8 83 RNA Photi	nus p	oyra <sup>-</sup>	lis											
<400> caucgac	8 uga a	aucco	cucco	c ug	guaau	ccg (	uuug	ggcu	cu g	cccug	cuau	ggg	auaaau	ıg	60
guuaucaggg auuuuagucg auc							83								
<210> <211> <212> <213>	9 62 RNA Photi	nus p	oyra <sup>-</sup>	lis											
<400> caucgac	9 :uga a	aucc	cuggi	ı aaı	uccgu	ugu	uaaca	aacg	ga u	uacca	ggga	uuu	caguco	ja	60
ug															62
<210> <211> <212> <213>	10 44 DNA Artif	icia <sup>^</sup>	l Sed	quen	ce										
<220> <223>	prime	r													
<400>	10 lact c	actai	tagg	a ca:	aggt <i>c</i> :	ata	atte	ctac	ca d	cta					44

1

	GNCA-P03-007SequenceListing.txt	
<210> <211> <212> <213>	11 44 DNA Artificial Sequence	
<220> <223>	primer	
<400> taatac	11 gact cactataggg cagatatttt cttaccaccc accc	44
<210> <211> <212> <213>	12 44 DNA Artificial Sequence	
<220> <223>	primer	
<400> taatac	12 gact cactataggg ttaagtttaa caggagaagc tgga	44
<210> <211> <212> <213>	13 44 DNA Artificial Sequence	
<220> <223>	primer	
<400> taatac	13 gact cactataggg aaatcattgc tttcctgata atgc	44
<210> <211> <212> <213>		
<220> <223>	primer	
<400> taataco	14 gact cactataggg tagatttccg cagccccagt gttc	44
<210> <211> <212> <213>	15 44 DNA Artificial Sequence	
<220> <223>	primer	
<400> taataco	15 gact cactataggg gttgcctctc atttttcctt gatt	44
<210> <211> <212> <213>	16 45 DNA Artificial Sequence	
<220> <223>	primer	

<400>	GNCA-P03-007SequenceListing.txt								
	gact cactataggg tattttagac tgattacttt tataa	45							
<211> <212>									
<220> <223>	primer								
	17 gact cactataggg tcacatgttt tggctaagac ctat	44							

**\*..**.